

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 03:31:18 ; Search time 8725 Seconds
(without alignments) 10984.305 Million cell updates/sec

Title: US-10-781-979-6

Perfect score: 1686

Sequence: 1 gtgagctcaagtacaa.....atcaagataaccgctaa 1686

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_in:*

3: gb_env:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pr:*

9: gb_ro:*

10: gb_scs:*

11: gb_sy:*

12: gb_un:*

13: gb_vl:*

14: gb_hcg:*

15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1686	100.0	1686	6	CQ868316
2	1686	100.0	5980	6	CQ868311
3	1466	87.0	3746	1	AB074414
4	1395.8	82.8	3727	1	AB074413
5	1335	79.2	4100	1	AB112346
6	970.4	57.6	3752	1	AB125059
7	941.4	55.8	3931	1	AB161456
8	914.8	52.3	4391	1	BTUEG65
9	891.4	52.9	3668	1	AB185105
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11	792.4	47.0	127823	1	BTBTOXIS
12	784.8	46.5	4186	1	BACISRH3
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ALIGNMENTS

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DEFINITION	CQ868316				
ACCESSION	CQ868316.1	GI:51998362			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Bacillus thuringiensis				
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	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus				
	cereus group.				

REFERENCE	1
AUTHORS	Carozzi,N., Hargiss,T., Koziej,M.G., Duck,N.B. and Carr,B.
TITLE	Delta-endotoxin genes and methods for their use
JOURNAL	Patent: WO 2004074462-A 17 02-SEP-2004;
	Athenix Corporation (US)

FEATURES

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Best Local Similarity 100.0%; Pred. No. 2.8e-236;

Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION CQ868311.1 GI:51998357
 KEYWORDS

SOURCE
 ORGANISM
 Bacillus thuringiensis
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 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
 1 Carozzi, N., Hargies, T., Koziel, M.G., Duck, N.B. and Carr, B.
 Delta-endotoxin genes and methods for their use
 Patent: WO 2004074462-A 12 02-SEP-2004;
 Athenix Corporation (US)

FEATURES
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 Bacillus thuringiensis serovar aizawai
 Bacillus thuringiensis serovar aizawai
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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 REFERENCE
 1 Ito, T., Sahara, K., Asano, S., and Bando, H.
 Cloning and Expression of Novel Crystal Protein Genes from Bacillus
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 JOURNAL
 TITLE
 AUTHORS
 Ito, T., Sahara, K., Asano, S., and Bando, H.
 DIRECT SUBMISSION
 JOURNAL
 Submitted (14-NOV-2001) Takeshi Ito, Graduate school of
 Agriculture, Hokkaido University, Kita-9-1you Nishi-9chome,
 Kita-ku, Sapporo-shi, Hokkaido 060-8589, Japan
 (E-mail: ito-c@ads.agr.hokudai.ac.jp, Tel: 81-011-716-2487)
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ORIGIN

Query Match 87.0%; Score 1466; DB 1; Length 3746;
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Matches 1570; Conservative 0; Mismatches 105; Indels 11; Gaps 3;

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LOCUS Bacillus thuringiensis serovar aizawai cry39A and 39orf2 genes for
DEFINITION mosquitocidal toxin and Cry39ORF2 protein, partial and complete
cde.
ACCESSION AB074413 GI:19386613
VERSION AB074413.2 GI:19386613
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Ito, T., Sahara, K., Bando, H. and Amano, S.
AUTHORS Cloning and Expression of Novel Cryetal Protein Genes cry39A and
TITLE 39orf2 from Bacillus thuringiensis subsp. aizawai Buni-14 Encoding
JOURNAL Mosquitocidal Proteins
REFERENCE Insect Biotechnol. Sericology 71, 123-128 (2002)
AUTHORS Ito, T., Sahara, K., Amano, S. and Bando, H.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2001) Takeshi Ito, Graduate school of
REFERENCE Agriculture, Hokkaido University, Applied Bioscience, Kita 9-Jyo,
AUTHORS Nishii 9-chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan
JOURNAL (E-mail: ito-teads.agr.hokudai.ac.jp, Tel: 81-011-706-2487,
Fax: 81-011-706-2487)
COMMENT On Mar 12, 2002 this sequence version replaced gi:16945768.
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ORIGIN
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LOCUS AB112346 4100 bp DNA linear BCT 14-JUN-2003
DEFINITION *Bacillus thuringiensis* serovar aizawai cry40-1-like and ORF2 gene
for putative mosquitocidal toxin, hypothetical protein, complete
cde.
ACCESSION AB112346
VERSION AB112346
KEYWORDS GI:31745043
SOURCE
ORGANISM *Bacillus thuringiensis* serovar aizawai
Bacillus thuringiensis serovar aizawai
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus*
cereus group.
REFERENCE
AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
TITLE Cloning and Expression of Novel Crystal Protein Genes from *Bacillus thuringiensis* subsp. aizawai Encoding Mosquitocidal Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4100)
AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2003) Takeshi Ito, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience, Kita-9-jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail: ito-t@abds.agr.hokudai.ac.jp, Tel: 81-11-706-2487 (ex. 2487))
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ORIGIN

Query Match 79.2%; Score 1335; DB 1; Length 4100;
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RESULT 6
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 LOCUS 3752 bp DNA linear BCT 28-OCT-2003
 DEFINITION Bacillus thuringiensis serovar entomocidus cry30Aa like gene for
 putative mosquitocidal toxin and hypothetical protein gene,
 complete cds.
 ACCESSION AB125059
 VERSION AB125059.1 GI:37999233
 KEYWORDS
 SOURCE Bacillus thuringiensis serovar entomocidus
 ORGANISM Bacillus thuringiensis serovar entomocidus
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
 cereus group.

REFERENCE
 1 Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Asano, S.
 Cloning and Expression of Novel Crystal Protein Genes from *Bacillus*
thuringiensis subsp. *entomocidus* INA288
 JOURNAL Unpublished
 2 (bases 1 to 3752)
 TITLE
 AUTHORS Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Asano, S. and Bando, H.
 DIRECT SUBMISSION
 JOURNAL Submitted (24-OCT-2003) Tomonori Ikeya, Graduate School of
 Agriculture, Hokkaido University, Department of Applied Bioscience,
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 (E-mail: ikeyan@agr.hokudai.ac.jp, Tel: 81-011-706-2487 (ex. 2487),
 Fax: 81-011-706-2487)
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Bacillus thuringiensis serovar entomocidus cry4Ba like and ORF2
genes for putative mosquitoicidal toxin and hypothetical protein,
complete cds.
ACCESSION
AB161456
VERSION
AB161456.1 GI:41688282
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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Ikeya,T., Yamaya,K., Ito,T., Sahara,K., Bando,H. and Asano,S.
Cloning and Expression of Novel Crystal Protein Genes from Bacillus
thuringiensis subsp. entomocidus INA288
JOURNAL
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AUTHORS
2 (bases 1 to 3931)
Tomonori,I., Kumiko,Y., Takeshi,I., Ken,S., Shin-ichiro,A. and
Hisanori,B.
Direct Submision
Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of
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(E-mail:ikeya@abds.agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487),
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VERSION cry19aA gene; mosquitocidal toxin; ORF2.
KEYWORDS Bacillus thuringiensis
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ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1
AUTHORS Rosso, M.L. and Delecluse, A.
TITLE Contribution of the 65-kilodalton protein encoded by the cloned gene cry19A to the mosquitocidal activity of Bacillus thuringiensis

JOURNAL subsp. jegathesan
PUBMED Appl. Environ. Microbiol. 63 (11), 4449-4455 (1997)
REFERENCE 9361431
2 (bases 1 to 4391)
AUTHORS Delecluse, A.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1996) A. Delecluse, Institut Pasteur, Unite des Bacteries Entomopathogenes, 25 rue du Dr. Roux, 75724 Paris Cedex 15, FRANCE
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VERSION	AB185105.1	GI:50539654			
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SOURCE	Bacillus thuringiensis				
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.				
REFERENCE	1				
AUTHORS	Ohgushi, A., Saitoh, H., Wasano, N. and Ohba, M.				
TITLE	Cloning and characterization of novel cry genes from a mosquitocidal Bacillus thuringiensis serovar sotto strain				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3668)				
AUTHORS	Ohgushi, A., Saitoh, H., Wasano, N. and Ohba, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JUL-2004) Akira Ohgushi, Kyushu University, Graduate School of Agriculture; 6-10-1, Hakozaki, Higashi-Ku, Fukuoka, Fukuoka 812-8581, Japan (E-mail: ohgushi@db.kyushu-u.ac.jp, Tel: 81-92-642-3028, Fax: 81-92-642-3028)				
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ORIGIN

Query Match 52.9%; Score 891.4; DB 1; Length 3668;
Best Local Similarity 74.2%; Pred. No. 4.3e-152;

Matches 1187; Conservative 0; Mismatches 391; Indels 21; Gaps 4;

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RESULT 10			
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DEFINITION	Bacillus thuringiensis gene for Cry3D-like, hypothetical protein,		
ACCESSION	AB193814		
VERSION	AB193814.1	GI:54695304	
SOURCE	Bacillus thuringiensis		
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1		
AUTHORS	Ohgushi,A., Wasano,N., Saitoh,H. and Ohba,M.		
TITLE	Identification and characterization of novel cry genes from an mosquito-specific Bacillus thuringiensis serovar sotto strain unpublished		
JOURNAL	2 (bases 1 to 3642)		
REFERENCES	Ohgushi,A., Wasano,N., Saitoh,H. and Ohba,M. Direct Submission Submitted (28-OCT-2004) Akira Ohgushi, Kyushu University, Graduate School of Agriculture, 6-10-1, Hakozaki, Higashi-Ku, Fukuoka, Fukuoka, 812-8581, Japan (E-mail: ohgushi@bbs.kyushu-u.ac.jp, Tel:81-92-642-3028, Fax:81-92-642-3028)		
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Query Match	49.8%	Score 839.6	Length 3642
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Db 2233	GAATATGATTAATATGGCAACCTATGTAATAAATATGCAATGAAACAATATTCACAA	2292	
QY 121	AAATATACTTATGGGATGAAATTAACCTGGCAAAACAACTTATAGCTCTCGAATCTA	180	
Db 2293	AAATATGATCAATGGAATGACATTAATATGCAACAACTTATAGCTCAAGCAGTAATTA	2352	
QY 181	CTCCAAATAGGAGACTT-----TTCGGGAATGATTTGACATTCGGTAATGATTTATC	234	
Db 2353	CTTCAAAATGATGATTTTGAAGATTATTTATGATGATGACCTACAGTAATCAGATGTC	2412	
QY 235	ATAGAGATCCAAATATCTATTTTAAAGAAATTTCTACAGATGCTGACGACGAC	294	
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QY	1003	TTGAACATATGATGATATATCAAGAGTTAAACGACATATCAGCAAGTTATTAATTATAT	1068
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Db	3610	GAAAGCATCGAATTACTTTGGCCGAAAGGATA	3641
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LOCUS	BTBPTOXIS	127923 bp	DNA
DEFINITION	Bacillus thuringiensis subsp. israelensis plasmid pBtoxis.	linear	BCT 16-APR-2005
ACCESSION	AL731825		
VERSION	AL731825.1	GI:21685410	
KEYWORDS			
SOURCE			
ORGANISM	Bacillus thuringiensis serovar israelensis Bacillus thuringiensis serovar israelensis Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1 (bases 1 to 127923)		
AUTHORS	Berry,C., O'Neil,S., Ben-Dov,E., Jones,A.F., Murphy,L., Quail,M.A., .. and Parkhill,J. Hoiden,M.T., Harris,D., Zaritsky,A. and Parkhill,J. Complete sequence and organization of ptoxis, the toxin-coding plasmid of Bacillus thuringiensis subsp. israelensis Appl. Environ. Microbiol. 68 (10), 5082-5095 (2002)		
JOURNAL	PUBMED	12324359	
REFERENCE	2 (bases 1 to 127923)		
AUTHORS	Parkhill,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-APR-2002) Submitted on behalf of the pBtoxis sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk		
COMMENT	Notes: Details of pBtoxis sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/B_thuringiensis/).		
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gene			
CDS			

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/note="1 probable transmembrane helix predicted for pBc006 by TMHMM2.0"
RBS complement(5515..5519)
gene complement(6451..8160)
/gene="pBc007"
CDS complement(6451..8160)
/gene="pBc007"
/note="Similar to Bacillus anthracis pxa1-16 TR:Q9X2Y7 (EMBL:AF065404) (569 aa) fasta scores: E(): 0, 96.13% id in 569 aa, and to Bacillus thuringiensis pxa1 orf16-1-like protein TR:CA050562 (EMBL:AJ296638) (310 aa) fasta scores: E(): 6.5e-122, 99.67% id in 310 aa"
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/db_xref="GI:21685416"
/db_xref="UniProt/TREMBL:Q8KX1"
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GLDGRYITKLTIFPMEETEKANPPIYISPVFTKQRFGLSTIAKKLFLDIMQCHTET
TLKRLSDQDERGNKTHFGMRFLPHKRYPHQIDRPIELTALCTSNPLKICMKG
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ELSDANKGFIHLVLYKTYCHQIRSVIRGLDMVDRREGPTKIVYTLKTLHQTSQYQI
LDTAKKEGIYPLAIOHIPKERNSDRGOAVFNGLHYSWYSLINKIRMPENVALKOK
FAVPTESSYRYNYLKQOETLFRYKAYIDOGYNLHAYIATLEIMBEKIKVGRKERTI
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EIK"
RBS complement(8168..8173)
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gene 8959..10653
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/note="Similar to Bacillus anthracis pxa1-14 TR:Q9X2Y5 (EMBL:AF065404) (564 aa) fasta scores: E(): 1.6e-191,
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Best Local Similarity 72.3%; Pred.No.14e-134;
Matches 1094; Conservative 0; Mismatches 396; Indels 24; Gaps 4;
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QY 61 GAAATAGATCAACGGCCATTTCCTATAGATGTATGTCAGATGAACAAATCTCTACGAA 120
DB 41206 GAAATAGATCAAGTGGCTATCTATAGATGTATGTCAGATGAACAAATCTCTACGAA 41265
QY 121 AAAATAGATTATGGAGTAAATAAATCGGAAACAACCTTAGTCAGTCTGATATCA 180
DB 41266 AAACGTAGTTATGGATCAACATTAACAATGCAAAATCTTAGTCAGTCTGAAATTTG 41325
QY 181 CTCCAAAATGAGACCTTTCTG-----GGAATGATGGACATTCGGTATGATATATC 234
DB 41326 CTTCAAAATGAGATTTTGAAGATGATATTCATGTAGTACGACATCAAGTATCATATGTC 41385
QY 235 ATAGATCCAAATATCTATTTTAAAGAAAAATTTCTACAGATGCGTGACACAGAGC 294
DB 41386 ATTCAGTCGATATATCTTCTTAAAGAAATTTATCGAATATATCTGGGCGGAGAC 41445
QY 295 ATATATGAGACTCTATTTCCAACTATATCTGTCAAAAATATGAGAGCTAAATTA 354
DB 41446 ATATATCTTAACGATATTTCCAACTATATCAAAAATATGAGAGCTAAATTA 41505
QY 355 CCATATACACGTTATCGAGTAGAGAGGTTTGGGAAAGTAGTAAGATTGAAATTAATG 414
DB 41506 CCGTATACACGTTATCTAGTAGAGGATTTTGGAGAAAGTAGTAAGATTGAAATTAATG 41565
QY 415 GTAACACGTTACGGGAAAAAATGATGCTATCATGAATGTTCCAAATGATTTGGCTAT 474
DB 41566 GTTTCACGCTATGAAAAAATATGATACAGTCATGAATGTCATTGATATCCGCTAT 41625
QY 475 ATGACAGCTTAATCTTCAATG-----GGAATATATCGTGTGAATCATCGTCAATG 528
DB 41626 GTATCTTTCAGGCCGTGTTGTATGATATATATGATGGAACAACAACCGATCCAAAT 41685
QY 529 GTGAGCAAGGATATCTTACCAACAGATGATATGCTC-----CGATATGATGCA 582
DB 41686 GGGATATGATATATATATATATCAATATGTCAGCTTTTACGCTTTCATCATCTGATGCT 41745
QY 583 TGCCCGCAAAATATATGATGAAAGATGGAAGTGAAGTCAAGATGTCATCATCTGATTTG 642
DB 41746 CGTCACTGATATCCAGGAAAAAACAAGATGCTGTCAAGATTCATCATGTTAAGTTC 41805
QY 643 CATATTTGACACCGGAGAGTATATCAAAATATATATGATATGATGATCTTATTA 702
DB 41806 CATATTTGATACAGGAGAT 41865
QY 703 ATTTCTAATCCAGATGATACGCTACAGTAGGAATCTAGAGTATGAAAGATGAAAGACCA 762
DB 41866 ATATCTTCCCGAGATGATATGATATATATATATATATATATATATATATATATATATAT 41925

Qy	763	CTAACAGGTGAAGCATTTGGCAGATGTGAACAAAGAAAAGAAATGGAACACACATG	822
Db	41926	ATAGATGGGAAAGCACTGTGACGCGTGAACCAATGGAAGAAATGGAACATCAATG	41985
Qy	823	GAGAAAAACGTTGGGAAACACACAAAGCCTATGATCCAGCAAAAAGGCTGTAGATCA	882
Db	41986	GAAAGCAAAACGTTGGGAAACACACAAAGCATATGATGACAAACAAAGCCATGATGCT	42045
Qy	883	TTATTACCAATGAACAAGA-----GTTACCTATCATATTACTTTAGATCATATTCA	936
Db	42046	TTATTCACAAAATGTCAAGATAGGCTTTACAGTTGATACACACACTCGCTCAAAATTGAG	42105
Qy	997	AACGCTGATCCAGCTGTACGTGATCCCTTATGATATCCATATGGTTACCGATGCT	996
Db	42106	TACGCTGATATTTTGTGATCAATGATTCATATGATGATCAATGATTTGTTCAAGATGTT	42185
Qy	997	CCAGGTATGAATCTATGATATATATCAAGATTTAAACGACGTATGATGCAAGGTTATAT	1056
Db	42166	CCAGGTATGAATATATGACATCTATATGATGATGACGAGTGACCAAGCGGTTAT	42225
Qy	1057	TTATATGATGACGCAAAATGTCATAACAAATGCTGCTTTACACAGATTTACAGGATGG	1116
Db	42226	TTGATGATACCAAGAAATATTAATAAATGCTGATTTTACACAAAGGGTAAATGGGCTGG	42285
Qy	1117	CACGCAACAGGAAATGCCGCGGTACACAAATGATGAGAGCTTCAGTATTAGTTCTATCA	1176
Db	42286	CATGTAATCTGAAATGACAGCATACACAAATGATGAGGTTTCTGATATGTTTATCT	42345
Qy	1177	AATGAGACGCGGGGGATCTTCAAAACCTTGACCTCAAGATCATCATGATATGTTTA	1236
Db	42346	AATGAGATGCTGGGATCTATCTCAAAATGTCATCTCAACATATCATGCGGATGTTCTTA	42405
Qy	1237	CGTGTGATTCGCAAAAAGAGACCTGGAAAAGGCTATGATACATGATGATGTTAT	1296
Db	42406	CGTGTATTTGCCAAAAGAAAGAGGCGCTGGAATGGGATGTCACCCCTTATGATGTGAG	42465
Qy	1297	GAAAAGCAGGAACCTTAAGTTCATCTTCTGCAAGAAAGATATATGACAAAACAGTA	1356
Db	42466	GAGATTCAGAAAATTTGACGTTTACGTTCTGTGAAAGAGATATATTCGAAAACAGTA	42525
Qy	1357	GAGGTATTCGCAAAAGTATCGTGTACGATTTGAATAGAGAAACGAAAGTATCTT	1416
Db	42526	GATGTATTCGCAAGATACAGATTTGTATCGAATTTGATAGAGAAACGAAAGTTCGTTT	42585
Qy	1417	TATATGATTAAGTGAAGTTCGTTTGTATGCAAGATATGATTAACATATATATCTGCAC	1476
Db	42586	TATATCGAAGCATTTGAATTAATTTGCATGACGATTAATGATTAATTAATAAAT	42645
Qy	1477	ACGGGTATATGTA 1490	
Db	42646	AAGATTTCTAGCTA 42659	

RESULT 12
BACISRH3 4186 bp DNA linear BCT 17-FEB-1998
LOCUS
DEFINITION Bacillus thuringiensis israelensis plasmid gene for 130 kDa
insecticidal protein (ISRH3), complete cds.
ACCESSION D00247
VERSION D00247.1 GI:216287
KEYWORDS 130 kDa insecticidal protein (ISRH3).
SOURCE Bacillus thuringiensis serovar israelensis
ORGANISM Bacillus thuringiensis serovar israelensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 4186)
Ser.K., Honda,G., Koyama,N., Nishida,M., Neki,A., Sakai,H.,
Himeno,M. and Komano,T.
Cloning and nucleotide sequences of the two 130 kDa insecticidal
protein genes of Bacillus thuringiensis var. israelensis
Agric. Biol. Chem. 52, 873-878 (1988)
The genes of ISRH3 and ISRH4 that were 130 kDa insecticidal

proteins of Bti were sequenced and compared with other insecticidal
protein genes. ISRH3 and ISRH4 were identical in a region of the
C-terminal 467 amino acids.

FEATURES

Location/Qualifiers

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/mol_type="genomic DNA"

/strain="HD522"

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/db_xref="taxon:1430"

/clone="pBGH3"

/plasmid="pBti-5 and pBti-6"

/note="Clai site"

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/note="Shine-Dalgarno sequence"

461..3868

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ORIGIN

Query Match 46.5%; Score 784.8; DB 1; Length 4186;
Best Local Similarity 68.2%; Pred. No. 9.5e-133;
Matches 1162; Conservative 0; Mismatches 512; Indels 30; Gaps 4;

Qy	1	GTGAGTCCTATGTTTACAGTAGTACGAAAATACTGTTAAATAATAGAAACGACAGATTAT	60
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Qy	61	GAAATAGATCAAGCGGCATTTCTATAGATATGTGTCAGATGAAACAAATCTTCAGGAA	120
Db	2474	GACATAGATCAAGCGGCAAACTTGTGGAAGTATTTCTGAAGATTAATATACCAAAAGAA	2533
Qy	121	AAATTAATGTAAGGATGGAATAAATCTGGCAAAACAACTTAGTACGTCTGTAATCTA	180
Db	2534	AAATGCTGTTATAGATGAAGTTAAATAATCGAAACAACTTATCATCTCGAAATGTA	2593
Qy	181	CTCCAAATGAGAGACTT-----TCTGGGAATGATTGACATTCGGTAATGATATTATC	234
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Qy	235	ATAGATCAATTAATCTTATTTTAAAGAAAATTTCTACAGATGCGTGAGCGACGAGAC	294
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Qy	295	ATATATGAATCTATTTCCAACTATATCTGCAAAAATATAGATGATGCTTAATTAATA	354
Db	2714	ATTGATGATGATATTTCCGACCTATATATTTCCAAAATATGATGATCAAAATTTAA	2773
Qy	355	CCATATACACGTTATCGAGTAAGAGGTTTGTGGGAAGTAAAGATTGAAATTAATG	414

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 Qy 415 GTAAACGTTACGGGAAAGAAATGATGCTATCATGATGTTCCAAATGATTTGGCTTAT 474
 Db 2834 GTTTACCGCTATGGGGAAAGAAATGTATGTCATCATGAAATGTTCCAGCTATTTAAACTAT 2893
 Qy 475 ATGCAGCTTAATCTTCATGATGGAGATTATCGCTGTGAATCATCGCTCATGATGTGAC 534
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 Qy 535 CAAGGATATCTTACACCAACAGATGGATATGCTCCGAGATATGATGATGATGCCGCAAAAT 594
 Db 2942 TCCGCTGTCGGGCTTACATTTGGAACTTCTGATATGTTGATTTCAATTCCTCAATATGAT 3001
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 Db 3002 AAGAGGAAAGAAACATGTGATGTCAGATGCCATTCATTTAGTTTCACTATTTGATACA 3061
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 Db 3062 GGGGCAATTAATATCAAAATATAATAGGGGTTGGGCTATGTTTAAAAATCTTCTCCA 3121
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Qy 1489 TATGACCAAGTATTAATGAAATTAATATCAAAATTAATGATGATGATGATGATGATGAT 1548
 Db 3902 GGAGAAAGTTTCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3961
 Qy 1549 TATACCAACATTAATACCAAGACCTTAG-----TAATATGATATATCAAAATTAATGAT 1602
 Db 3962 TATGACCAACATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4021
 Qy 1603 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662
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 Db 4082 TGTGATCCAGATTAATGATGATGAT 4105
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 E01905
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 ACCESSION E01905
 VERSION E01905.1 GI:2170154
 KEYWORDS JP 1989080294-A/1.
 SOURCE JP 1989080294-A/1.
 ORGANISM *Bacillus thuringiensis*
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*
 cereus group.
 REFERENCE 1 (bases 1 to 4186)
 AUTHORS Komano, T. and Himeno, M.
 TITLE BT INSECTICIDAL PROTEIN GENE
 JOURNAL Patent: JP 1989080294-A 1 27-MAR-1989;
 SUMITOMO CHEM CO LTD, MARUBENI CORP
 COMMENT OS *Bacillus thuringiensis*
 PN JP 1989080294-A/1
 PD 27-MAR-1989
 PE 21-SEP-1987 JP 198728394
 PI KOMANO TORU, HIMENO MICHIO
 PC C12N15/00, A01N63/00, C07K13/00, C12N1/20, C12P21/02, (C12P21/02,
 C12R1:19);
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 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
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 FT CDS 461..3868
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 /mol_type= "genomic DNA"
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 ORIGIN
 Query Match 46 5%; Score 784.8; DB 6; Length 4186;
 Best Local Similarity 68.2%; Pred. No. 9.5e-133;
 Matches 1162; Conservative 0; Mismatches 512; Indels 30; Gaps 4;
 Qy 1 GTGAGTCTATGTTTACAGTAGTACGAAATAAGTTAAATAAGAAACGACAGATTAT 60
 Db 2414 GTGAATGACATGTTTAAATAGACGGAAGATGATTTAAACATTTGGAACGACAGATTAT 2473
 Qy 61 GAAATGATCAAGCGGCAATTTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 120

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Qy      121  AAATAATATGTTATGGAGATGAAATTAACCTGGCAAAACAATTAGTCACTCTGCTATCTA 180
Db      2534 AAAATGCGTTATATGATGAAAGTTAAAAATGGAAACAATTAGTCAATCTCGAATGTGA 2593
Qy      181  CTCCAAAATGGAAGACTT-----TCTGGGAATGATGGACCTTGGATGATGATTTATC 234
Db      2594 CTTCAAAACGGGGATTTTGAATCGGCTACGCTTGGGTTGGACACAAGATGATATATCA 2653
Qy      235  ATAGATCAATTAATCTATTTTAAAGAAAATTTCTACAGATCGTGAGACAGAGAC 294
Db      2654 ATTCAAGAAAGATGATCTATTTTAAAGGCAATTACTTCAATATCTCGGGCGAGAGAC 2713
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Db      2714 ATTGATGGTACGATATTTCCGACTATATATTTCCAAAAATTTGATGAATCAAAATTA 2773
Qy      355  CCATATACAGTTATCGAGTAAGAGGTTTGGGAGATGATGAAGATTTGAATTAATG 414
Db      2774 CCGATACAGTTACTTATGTAAGGGATTTGTAGAAATGTAAGATGTAAGACTAGTG 2833
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Db      2834 GTTTCAGCTATGGGGAAGAAATTTGATGCATCATGAATGTTCCAGTGAATTAATCTAT 2893
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Qy      655  GGAAGATGATATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
Db      3062 GGGGCAATGATATCAAAATGAAATATAGGGTTGGGTCATGTTTAAATATCTTCTCCA 3121
Qy      715  GATGATACGCTACAGTAGGGAATCTAGAGTCAATGATGATGATGATGATGATGATGAT 774
Db      3122 GATGATACGCTACATTTGATATTTAAGATTAATGTAAGAGGCAATGATGATGATGAT 3181
Qy      775  GCATTTGCAATGTGAAACAAAAGGAAAGAAATGGAACAACATGAGAGAAAAAGCT 834
Db      3182 GCATGTCAAGCGGTGAACACATGGAAGAAATGGAACGATCAAAATGGAAGCAAAAGCT 3241
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Qy      949  CTGTACAGTGTATCTCTATGTATACATATTTGGTATCCGAATGCTCCAGATATGAC 1008
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Db      3602 GGGGTATCTGAAATGTCCATCTCAACATATATGATGATGATGATGATGATGATGATG 3661
Qy      1249  AAAAAAGAGACCTGGAAAAAGGATATGTAACGATGATGATGATGATGATGATGATGAT 1308
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Db      3722  AAATTTGACGTTTACGCTCTTGGAAAGAGATATATTTACGAAGACATGATGATTTCCCA 3781
Qy      1369  GAAAGTATCGTGTACGATTTGAAATTTGAGAAACCGAAGGTACATTTTATATGATAGC 1428
Db      3782  GATACAGTGTGTACGAATTTGAGATGAGCAAAACGAAGGTTGTTTATATGAAAGC 3841
Qy      1429  ATCGATTTGTTTATGCAAGATATGATATATATATATATATATATATATATATATATG 1488
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Db      4082  TGTATCAAGGATTAATGATTA 4105

RESULT 14
BRITOX
LOCUS      3684 bp      DNA      linear      BCT 18-APR-2005
DEFINITION      Bacillus churingiensis gene for 130 kDa delta-endotoxin.
ACCESSION      X07082
VERSION      X07082.1 GI:40309
KEYWORDS      endotoxin; insecticidal protein.
SOURCE      Bacillus churingiensis
ORGANISM      Bacillus; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE      1 (bases 1 to 3684)
AUTHORS      Tunpradubkul,S., Setteabaien,C. and Panyim,S.
TITLE      The complete nucleotide sequence of a 130 kDa mosquitto-larvicidal delta-endotoxin gene of Bacillus churingiensis var. israelensis
JOURNAL      Nucleic Acids Res. 16 (4), 1637-1638 (1988)
PUBMED      2831510
COMMENT      Data kindly reviewed (13.June 1988) by S. Panyim.
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ORIGIN

Query Match 46.5%; Score 783.2; DB 1; Length 3684;

Beet Local Similarity 72.2%; Pred. No. 1.9e-132;

Matches 1070; Conservative 0; Mismatches 388; Indels 24; Gaps 3;

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DB 2227 AAAATGCTTATTAAGTAGAATTAATAATGCAAACTTACGCTCGTATATCTA 2286
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QY 235 ATAGATCCAAATATCTATTTTAAAGAAATTTCTACAGATGCTGAGACAGAGAC 294
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DB 2467 CCGTATPACAGTTATCGAGTAAAGGGATTTGTAAGGAAGTAAAGATTTAAGAACTAGTG 2526
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DB 2587 CTGTATCTCTTAC-----CTTTGATTTGGAAGGATCTTAATGTTGTGAGACG 2634
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QY 595 ATAGATAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
DB 2695 AATAGATAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2754
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DB 3475 GAT 3534
QY 1429 ATGAGTGTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
DB 3535 ATGAT 3576

RESULT 15
BTTOXD2
LOCUS BTTOXD2 3684 bp DNA linear BCT 18-APR-2005
DEFINITION Bacillus thuringiensis israelensis bt8 gene for 130 kDa crystal protein (mosquito-specific toxin).
ACCESSION X07423
VERSION X07423.1 GI:40353
KEYWORDS delta-endotoxin; endotoxin; toxin.
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3684)
ChungJatupornchai, W., Hofte, H., Seurinck, J., Angsuthanasombat, C. and Vaecck, M.
Common features of Bacillus thuringiensis toxins specific for Diptera and Lepidoptera
Eur. J. Biochem. 173 (1), 9-16 (1988)
JOURNAL PUBMED 283395
COMMENT Data kindly reviewed (14-FEB-1989) by ChungJatupornchai W.

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Matches 1070; Conservative 0; Mismatches 388; Indels 24; Gaps 3;		
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Db	2413	ATTGATGATGAGATATTTCCGACCTTAATATTTCCAAAAATTTGATGATCAAAATTTAAA 2472
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Qy	775	GCATTGGCACTGTGAACCAAAAAGAAATGAAACAACATGAGAGAAAAAAGT 834
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Db	3301	GGCGTATCTCAAAATGTCAATCTTCACAAATATCATATGAGTATGCTTACGTTATTTGCC 3360
Qy	1249	AAAAAAGAGACCTGGAAAAAGGTATGTAACGATGATGATTTGTAATGAAACAGAGAA 1308
Db	3361	AAAAAAGAGACCTGGAATATGGTATGTCAAGCTTATGATTTGTAGAGAAATCAAGAA 3420
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Qy 1369 GAAAGTATCGTGTACGATTGAAATAGAGAAACCGAAGTACATTTTATATAGATAGC 1428
Db 3481 GATACAGATCGTGTACGATTGAGATAGGCGAAACCGAGTTGTTTATATCGAAMGC 3540
Qy 1429 ATCGAGTGTCTTGTATGCAAGATATGATTAACAATTAATPAC 1470
Db 3541 ATTGAATTATTTGCAATGACAGAGTGATTATTAATAAATAATPAC 3582

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Job time : 8728 secs

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GenCore version 5.1.7
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Total number of hits satisfying chosen parameters: 82156650

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	66	3.9	429	10	CG803197 1118039H0
5	63.6	3.8	241	10	CG807338 1118080H1
6	62.6	3.7	311	10	CG807109 1118077H0
7	62.4	3.7	430	10	CG803196 1118039H0
8	62	3.7	400	10	CG807323 1118080G0
9	61.8	3.7	707	10	CG187604 104_607_1
10	61.4	3.6	519	3	BI814949 PFEST0A0
11	60.8	3.6	471	10	CG807194 1118078H0
12	60.8	3.6	661	10	CG327486 104_823_1
13	60.8	3.6	697	8	DN635195 Cm mx0_43
14	60.8	3.6	712	8	DN738989 Cm mx0_51
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16	60.4	3.6	889	10	CG973509 ARAA-aaas
17	60.2	3.6	751	9	BZ063018 11a15b12
18	60	3.6	713	9	AZ217550 Sheared D
19	59.8	3.5	652	9	AO160770 nbxb0005P
20	59.8	3.5	662	9	AO051253 nbxb0001C
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26	59.6	3.5	700	9	BZ421879 1d46h10.b
27	59.4	3.5	426	10	CG289335 104_768_1
28	59.2	3.5	352	10	CG965330 ARAA-aaal
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30	59	3.5	401	9	BZ781689 1130h08.b
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33	59	3.5	891	10	CG952279 TC838.1.B
34	58.8	3.5	243	10	CG807203 1118078H1
35	58.8	3.5	231	10	CG807338 1118080H1
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37	58.8	3.5	773	9	BH319159 AG-ND-160
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39	58.4	3.5	755	10	CMS01883 fbbd001f2
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41	58.4	3.5	830	7	CK398276 AGENCOURT
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43	58.2	3.5	518	10	CG086559 PUCQ11TD
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ALIGNMENTS

RESULT 1
LOCUS CG807096 302 bp DNA linear GSS 10-NOV-2003
DEFINITION 1118077G01.y1 1118 - Rescuemu Grid S Zea mays genomic, genomic survey sequence.
ACCESSION CG807096
VERSION CG807096.1 GI:38244598
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 302)
AUTHORS Walbot,V.
TITLES Maize genomic sequences found using engineered Rescuemu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1118077 column: 2
Class: transposon-tagged.
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/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transgenic Mu units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 4.0%; Score 67.6; DB 10; Length 302;
Best Local Similarity 56.2%; Pred. No. 3.3e-05;
Matches 127; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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QY 1574 CTAGTAATATGTATTAATCAAAATTAATTAATTAATTAATTAATTAATTAATTT 1633
DB 171 ATATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 230
QY 1634 GTAACCAAGGCATTAATCTGCTGTACATGATCAAGATATTA 1679
DB 231 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 276

RESULT 2
CG807194 471 bp DNA linear GSS 10-NOV-2003
LOCUS 111807801.y1 1118 - Rescuemu Grid S Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CG807194
VERSION CG807194.1 GI:38244754
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 471)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1118078 column: 2
Class: transposon-tagged.
Location/Qualifiers
1..471
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="1118 - Rescuemu Grid S"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site: 1: BamHI, Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

ampicillin."

Query Match 4.0%; Score 67.6; DB 10; Length 471;
Best Local Similarity 56.2%; Pred. No. 3.6e-05;
Matches 127; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1454 ATGATACAAATTAATACCTGCACACGGGTATATGTATGACCAAGTTATATGAAATT 1513
DB 126 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 185
QY 1514 ATATCAAAATCTAGCGATGTATACCAAGGTATACCAACATCAACCAAGACT 1573
DB 186 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 245
QY 1574 CTAGTAATATGTATTAATCAAAATTAATTAATTAATTAATTAATTAATTAATTT 1633
DB 246 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 305
QY 1634 GTAACCAAGGCATTAATCTGCTGTACATGATCAAGATATTA 1679
DB 306 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 351

RESULT 3
CG807311 363 bp DNA linear GSS 10-NOV-2003
LOCUS 1118080F01.y1 1118 - Rescuemu Grid S Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CG807311
VERSION CG807311.1 GI:38244939
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 363)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1118080 column: 3
Class: transposon-tagged.
Location/Qualifiers
1..363
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="1118 - Rescuemu Grid S"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

FEATURES
source
1..471
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="1118 - Rescuemu Grid S"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site: 1: BamHI, Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

FEATURES
source
1..363
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="1118 - Rescuemu Grid S"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

[illegible]

and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 3.7%; Score 62.4; DB 10; Length 430;
Best Local Similarity 53.8%; Pred. No. 0.0062;
Matches 129; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 1440 TTGATGCAAGATGATGATACATATATATACCTGCACACGGGTATATGAGCAANG 1499
DB 277 TTATAGGAGTACTTAT 218
QY 1500 TTATATGGAATTTATATCAAAATCTAGCATGTCTTACCAAGGATATACAAACA 1559
DB 217 TTAT 158
QY 1560 CTATTAACCAAGCTAGTATATATATATATATATATATATATATATATATATAT 1619
DB 157 TTAT 98
QY 1620 TTCGGTTCACATGTATACCAAGGCAATCTGCTGTACATGTATCAAGATATTA 1679
DB 97 TTAT 38

RESULT 8
CG807323 400 bp DNA linear GSS 10-NOV-2003
LOCUS 1118080G01.Y1 1118 - Rescuemu Grid S Zea mays genomic, genomic
DEFINITION survey sequence.

ACCESSION CG807323
VERSION CG807323.1 GI:38244959
KEYWORDS GSS.

SOURCE

Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 400)
Maize genomic sequences found using engineered Rescuemu transposon
Unpublished (2001)

AUTHORS

JOURNAL

COMMENT

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 723 8221
Email: walbot@stanford.edu
Plate: 1118080 column: 3
Clas: transposon-tagged.
Location/Qualifiers

FEATURES

source

1..400
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Mixed Background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1118 - Rescuemu Grid S"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

ampicillin."

ORIGIN

Query Match 3.7%; Score 62; DB 10; Length 400;
Best Local Similarity 57.1%; Pred. No. 0.0076;
Matches 113; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1416 TTATATAGTACCATCGAGTCTTGTATGCAAGATATGATTAATTAATTAACCTGCA 1475
DB 148 TTAT 207
QY 1476 CACGGTATATATATATGAGCAAGATTAATGAATTAATTAATTAATTAATTAAT 1535
DB 208 TTAT 267
QY 1536 GTATTAACCAAGGATATACCAAGCTATTAATTAATTAATTAATTAATTAAT 1595
DB 268 TTAT 327
QY 1596 TTATATTAACATGATGA 1613
DB 328 TTAT 345

RESULT 9
CW187604/c 707 bp DNA linear GSS 30-OCT-2004
LOCUS 104_607_11172560.148 36727_032 Sorghum methylation filtered library
DEFINITION (LibID: 104) Sorghum bicolor genomic clone 11172560, genomic survey
sequence.

ACCESSION CW187604
VERSION CW187604.1 GI:54895932
KEYWORDS GSS.

SOURCE

Sorghum bicolor (sorghum)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 707)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korfi,I.F.,
Rabinowicz,P.D., Lakey,N., McCombe,W.R., Jeddelloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)

AUTHORS

JOURNAL

COMMENT

Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 607 row: b column: 08
Seg primer: SWfor Forward
Clas: methylation filtered
High quality sequence stop: 707.
Location/Qualifiers

FEATURES

source

1..707
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"
/db_xref="taxon:4558"
/clone_lib="11172560"
/clone_lib="Sorghum methylation filtered library (LibID: 104)"
/note="Organ: leaf; Vector: pBSC(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSC(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match	Similarity	3.7%	Score 61.8	DB 10	Length 707
Best Local	Similarity	51.6%	Pred. No. 0.00093		
Matches 141	Conservative	0	Mismatches 132	Indels	Gaps 0
Oy	1413	ATTATTATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATATGATTAACAATTAATTAACCT	1472		
Db	301	ATTGAATATATTATATATATTCCTATTAATTTGCTATTACATATATATATTAATTAATTAATTA	242		
Oy	1473	GCACACGGGTATATATGTTATGACCAAGTTAATGGAATTTATATTCAAAATACATGACGA	1533		
Db	241	TAAATATATATATATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	182		
Oy	1533	TGTGATTATACCAAGGGTATATACAAACAATATACCAAGCTCTAGTAAATATGTTATTAATCA	1592		
Db	181	TAAATATATACAAACAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC	122		
Oy	1593	AAATTATATCTAACAAATGATGACCTTCGATTCGGTTGCAATGTAACCAAGGCATTAATCTC	1655		
Db	121	TAAATATACATTAACAATTAATTAACAACAATTAACAATGACATTAACAACAGATTAACAACAG	62		
Oy	1653	TGGCTGTACATGTATATCAAGATTAATTAACCGTTA	1685		
Db	61	TAAACAAGAACGTAAACAATTAACAATTAACAATTAACAATTA	29		
RESULT 10					
BI814949					
LOCUS	BI814949	519 bp	mRNA	linear	EST 03-OCT-2001
DEFINITION	PIEST00a08c12.y1	Plasmodium falci-parum 3D7 asexual cDNA	Plasmodium		
ACCESSION	BI814949				
VERSION	BI814949.1	GI:15907816			
KEYWORDS	EST				
SOURCE	Plasmodium falci-parum 3D7				
ORGANISM	Plasmodium falci-parum 3D7				
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
AUTHORS	1 (bases 1 to 519)				
	Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D.,				
	Matta, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B.,				
	Bowers, Y., Gibbons, M., Ritzer, E., Bennett, J., Jentes, B., Ronko, I.,				
	Tsagaris, S., R., Belaygorod, L., Franklin, C., Carr, L., Grow, A.,				
	Maguire, L., Ritchey, J., Wadkin, J., Kennedy, S., Levanso, D.,				
	Waterson, R., Wilson, R. and Sibley, D.				
TITLE	Washu Plasmodium EST Project				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: L. David Sibley				
	Washu Plasmodium EST Project				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA				
	Tel: 314 286 1800				
	Fax: 314 286 1810				
	Email: est@watson.wustl.edu				
	Library was constructed by Debopam Chakrabarti DNA sequencing by:				
	Washington University Genome Sequencing Center for information on				
	obtaining a clone please contact: L. David Sibley				
	(sibley@borcim.wustl.edu), Washington University				
	Seq primer: -40up from Glibco				
	High quality sequence stop: 421.				
FEATURES	Location/Qualifiers				
Source	1..519				
	/organism="Plasmodium falci-parum 3D7"				
	/mol_type="mRNA"				
	/db_xref="taxon:36329"				
	/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"				
	/clone_lib="Plasmodium falci-parum 3D7 asexual cDNA"				
	/note="Vector: pBluescript SK plus; Site 1: EcoRI; Site 2				
	XhoI; Library was constructed by Debopam Chakrabarti.				
	Total RNA samples were isolated from mixed stage				
	sapoin(0.1%)-lysed P. falci-parum 3D7 infected				
	erythrocytes by the acidic guanidinium-phenol chloroform				
	method. The poly A+ RNA was isolated by the polyAT-tract				
	RNA isolation system (Promega, WI) using streptavidin				

Mammosphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A) + RNA (5mg) into EcoRI and XhoI sites of 1 λ ZapII vector using the Zap cDNA synthesis kit (Stratagene, CA). The average size of the cDNA inserts in the library was between 1.0 and 1.5 kb. Clones were mass excised using the Exsist helper phage (Stratagene), the phagemid were preplated with pG3 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."

Query Match	3.6% ; Score 61.4 ; DB 3 ; Length 519 ;
Best Local Similarity	51.7% ; Pred. No. 0.0011 ;
Matches 140 ;	Conservative 0 ; Mismatches 131 ; Indels 0 ; Gaps 0 ;
Oy	1415 TTATATATAGATAGCATCGAGTTGCTTTGTATGCAAGATATGATTAACAATATTAACCTGC 1474
Db	39 TTATATATGATTAATATGGAATTCATCATTAATTAATGATTAATTAATTAATTAATTAATTA 98
Oy	1475 ACACGGTATATGCTATAGCAAGTAAAGTTAAATGAAATTATTAATCAAAATTAATAGCATG 1514
Db	99 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 158
Oy	1535 TGTATTACCAAGGGTATATACAAACAATATTAACCAAGACTCTAGTAAATATGTAATCAAA 1594
Db	159 ATATATTAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 218
Oy	1595 ATTAATCTAACATGATGATGACCTGCATTCGCGTGGACATGTAACCAAGGCATTAACCTG 1654
Db	219 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 278
Oy	1655 GCTGTACATGTAATCAAGATTAATTAACGGTTA 1685
Db	279 GTGCTCCTTAATTAATTAATGCTGTGTAATTA 309
RESULT 11	
CG807194/c	471 bp DNA linear GSS 10-NOV-2003
LOCUS	1118078H01.Y1 1118 - RescueMu Grid S Zea mays genomic, genomic
DEFINITION	Survey sequence.
ACCESSION	CG807194
VERSION	CG807194.1 GI:38244754
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 471)
TITLE	Maize genomic sequences found using engineered RescueMu transposon
JOURNAL	Unpublished. (2001)
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 723 8221 Email: walbot@stanford.edu Plate: 1118078 column: 2 Class: transposon-tagged. location/Qualifiers 1. 471 /organism="Zea mays" /mol_type="genomic DNA" /cultivar="mixed background W23/A188/B73" /db_xref="taxon:4577" /tissue_type="leaf" /dev_stage="adult" /lab_host="DH108" /clone_id="1118 - RescueMu Grid S" /note="Organ: leaf; Vector: RescueMu (engineered from
FEATURES	
source	

/tissue_type="Gill, hypodermis, heart, hepatopancreas, antennal gland, brain, testis, muscle"
/dev_stage="Adult"
/clone_lib="Green Shore Crab Multiple Tissue, Normalized"
/note="Vector: PCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, then pooled for construction and normalization of the cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at the Center for Marine Functional Genomic Studies, Mount Desert Island Biological Laboratory (J.N. Forrest, Jr., Director). Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software). The project was supported by NIH Grant Number P20-RR-16463 from the INBRE Program of the National Center for Research Resources (P.H. Hand, PI)."

ORIGIN

Query Match 3.6%; Score 60.8; DB 8; Length 697;
Best Local Similarity 56.5%; Pred. No. 0.0016;
Matches 113; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

OY 1414 TTTTATATAGATGATCGAGTTCCTTGTATGCAAGATATGATACATATACCTG 1473
DB 564 TTCTAAAGGAAGACATATATTTATATATATGATATATATATATAT 505
OY 1474 CACACGGGTATATGTATGCAAGATTATATGAAATTATATCAAAATCTGCAT 1533
DB 504 AAT 445
OY 1534 GTGATTACCAAGGTATACCAACTATACCAAGCTAGTATATATATATCA 1593
DB 444 TATTTATTTATATATATATATATATATATATATATATATATATATAT 385
OY 1594 AATTATCTAACATGATGA 1613
DB 384 AATATATATATATATATATAT 365

RESULT 14
DN738989/c 712 bp mRNA linear EST 31-MAR-2005
LOCUS DN738989
DEFINITION Cm mx0.51h03 SP6 Green Shore Crab Multiple Tissue, Normalized
Carcinus maenas cDNA clone Cm mx0.51h03.5, similar to
ref|NP_307078.1| TRANSLOCASE PROTEIN IATC HOMOLOG - Molinella
succinogenes DSM 1740. Score = 33.9 bits (76), Expect = 4.0, mRNA
sequence.
DN738989
ACCESSION DN738989.1 GI:62115999
VERSION DN738989.1
KEYWORDS EST.
SOURCE Carcinus maenas (green crab)
ORGANISM Carcinus maenas
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidae; Portunidae; Carcinus.

REFERENCE 1 (bases 1 to 712)
Towle,D.W. and Smith,C.M.
Expressed sequence tags in a normalized cDNA library prepared from
multiple tissues of adult green shore crab, Carcinus maenas
Unpublished (2005)
JOURNAL Contact: David W. Towle
Marine DNA Sequencing and Analysis Center
Mount Desert Island Biological Laboratory
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
Tel: 207-288-9880 x474
Fax: 207-288-2130
Email: dtowle@mdibl.org
Plate: 51 row: h column: 03
Seq primer: SP6
High quality sequence stop: 508.
Location/Qualifiers
1..712

FEATURES
source

/organism="Carcinus maenas"
/mol_type="mRNA"
/db_xref="taxon:6759"
/clone="Cm mx0.51h03"
/tissue_type="Gill, hypodermis, heart, hepatopancreas, antennal gland, brain, testis, muscle"
/dev_stage="Adult"
/clone_lib="Green Shore Crab Multiple Tissue, Normalized"
/note="Vector: PCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, then pooled for construction and normalization of the cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at the Center for Marine Functional Genomic Studies, Mount Desert Island Biological Laboratory (J.N. Forrest, Jr., Director). Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software). The project was supported by NIH Grant Number P20-RR-16463 from the INBRE Program of the National Center for Research Resources (P.H. Hand, PI)."

ORIGIN

Query Match 3.6%; Score 60.8; DB 8; Length 712;
Best Local Similarity 56.5%; Pred. No. 0.0016;
Matches 113; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

OY 1414 TTTTATATAGATGATCGAGTTCCTTGTATGCAAGATATGATACATATACCTG 1473
DB 564 TTCTAAAGGAAGACATATATTTATATATATGATATATATATATATAT 505
OY 1474 CACACGGGTATATGTATGCAAGATTATATGAAATTATATCAAAATCTGCAT 1533
DB 504 AAT 445
OY 1534 GTGATTACCAAGGTATACCAACTATACCAAGCTAGTATATATATATCA 1593
DB 444 TATTTATTTATATATATATATATATATATATATATATATATATATAT 385
OY 1594 AATTATCTAACATGATGA 1613
DB 384 AATATATATATATATATATAT 365

RESULT 15
BX139987 844 bp DNA linear GSS 13-MAR-2003
LOCUS BX139987
DEFINITION Danio rerio genomic clone DKEX-99E7, genomic survey sequence.
ACCESSION BX139987
VERSION BX139987.1 GI:27971314
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 844)
Humphray,S.J., Huckle,E. and Durham,J.L.
Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humphray@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 99E7. 99E7 is
part of the Daniokey BAC library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/projects/D_rerio/.
Location/Qualifiers
1..844

FEATURES
source
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-99E7"
/tissue_type="Testis"

ORIGIN /note="vector pindigobAC-536"

Query Match 3.6%; Score 60.8; DB 10; Length 844;
Best Local Similarity 51.9%; Pred. No. 0.0017;
Matches 137; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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QY 1416 TTATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATATGATTAACAATATATACCTGCA 1475
    |||||
DB 493 TAAATATGATATATTTGATGATPAATPAATPAATGATATATATATATATATATATATATATAT 552
    |||||
QY 1476 CACGGTAAATNGTATGACCAAGTTAATTAATGAAATTATATCAAAATACTAGGATGT 1535
    |||||
DB 553 TAAATGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 612
    |||||
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DB 613 TAAATGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 672
    |||||
QY 1596 TTATACCTAACATGATGACCTGCAATTCGGTTGCAATGTAACCAAGGCAATTAATCTTGG 1655
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DB 673 TAAATATATATATGATGATPAATPAATPAATGATATCTAATATATGACCAATPAATPAATGA 732
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QY 1656 CTGTACATGATATCAAGATATTA 1679
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DB 733 CAATPAATATATATATATATATAT 756
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Search completed: February 15, 2006, 05:32:47
Job time : 7114 secs

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 03:24:57 ; Search time 1063 Seconds
(without alignments)
10570.717 Million cell updates/sec

Title: US-10-781-979-6

Perfect score: 1686

Sequence: 1 gtgagctcatgcttacaag.....atcaagatataaccgttaa 1686

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapept 1.0

Searched: 4996997 seqs, 332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*
14: geneeqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1686	100.0	1686	13	Adt89405 AXMT-0080
2	1686	100.0	5980	13	Adt89400 AXMT-008
3	914.8	54.3	4391	14	Aea61394 Bacillus
4	784.8	46.5	3684	1	Aan82106 Sequence
5	783.2	46.5	3684	6	Abk14949 Bacillus
6	783.2	46.5	3684	14	Aea61392 Bacillus
7	783.2	46.5	4065	1	Aan92515 Sequence
8	781.6	46.4	3535	1	Aan91003 Sequence
9	776	46.0	4184	1	Aan96139 Bacillus
10	772.6	45.8	4934	1	Aan81490 Insectici
11	763.8	45.3	3543	2	Aa081178 B.t. toxi
12	762.2	45.2	3543	2	Aa014669 Dipicran
13	708.2	42.0	10974	1	Aan60055 VB131 C10
14	637.8	37.8	4471	1	Aan93059 Delta-end
15	448.6	26.6	3940	1	Aan93054 Delta-end
16	384.2	22.8	4359	8	Abx13486 B. popilli
17	384.2	22.8	4359	14	Aeb90814 Paenibaci
18	379	22.5	3690	6	Abk51132 cDNA enco
19	357.4	21.2	3797	2	Aa036866 Coleopter

ALIGNMENTS

20	357.4	21.2	3797	2	Aa058975
21	331	19.6	3756	1	Aan50525
22	315	18.7	3471	2	Aa051704
23	313	18.6	4896	6	Aa043974
24	313	18.6	4896	10	Adf31301
25	313	18.6	4896	10	Adf31306
26	312.8	18.6	4366	8	Abx13497
27	312.8	18.6	4366	14	Aeb90830
28	311.8	18.5	3471	2	Aa030821
29	311.8	18.5	3471	2	Aa027167
30	311.8	18.5	3471	2	Aa028940
31	311.8	18.5	3471	2	Aa036653
32	311.8	18.5	3471	2	Aa043222
33	306.4	18.2	4359	8	Abx13496
34	306.4	18.2	4359	14	Aeb90828
35	306.2	18.2	4004	2	Aa005680
36	304.6	18.1	3414	2	Aa056922
37	303	18.0	3414	2	Aa041745
38	302.6	17.9	3621	6	Abk87234
39	302.6	17.9	3621	12	AdL15304
40	302.6	17.9	3621	14	Aeb45606
41	302.6	17.9	3621	14	Aeb34684
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ID	ADR89405 strand, cDNA, 1686 BP.
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XX	ADR89405;
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DT	18-NOV-2004 (first entry)
XX	
DE	AXMT-008orf2 coding sequence.
XX	
KW	ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW	expression cassette; transformation; transgenic; plant; bacteria;
KW	lepidoptera; coleoptera; pest; pesticide; resistance;
KW	pesticidal activity.
XX	
OS	Bacillus thuringiensis.
XX	
FT	
FT	Key
FT	CDS
FT	Location/Qualifiers
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FT	/product= "AXMT-008orf2"
FT	/transl_except= pos:1..3, aa:Met
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XX	MO2004074462-A2.
XX	
XX	02-SEP-2004.
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XX	
XX	20-FEB-2004; 2004MO-US005829.
XX	
XX	20-FEB-2003; 2003US-0448632P.
XX	20-FEB-2003; 2003US-0448633P.
XX	20-FEB-2003; 2003US-0448797P.
XX	20-FEB-2003; 2003US-0448806P.
XX	20-FEB-2003; 2003US-0448810P.
XX	20-FEB-2003; 2003US-0448812P.
XX	20-FEB-2003; 2004US-00781979.
XX	19-FEB-2004; 2004US-00782020.
XX	19-FEB-2004; 2004US-00782026.
XX	19-FEB-2004; 2004US-00782141.
XX	19-FEB-2004; 2004US-00782157.
XX	19-FEB-2004; 2004US-00782570.
XX	19-FEB-2004; 2004US-00783417.
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XX	Aag58975 B. thuring
XX	Aan50525 Bacillus
XX	Aa051704 Bacillus
XX	Aa043974 Bacillus
XX	Adf31301 Bacillus
XX	Adf31306 Bacillus
XX	Abx13497 B. popilli
XX	Aeb90830 Paenibaci
XX	Aa030821 Toxin 50C
XX	Aa027167 Delta-end
XX	Aa028940 B. thuring
XX	Aa036653 Bt isolat
XX	Aa043222 Antiscara
XX	Abx13496 B. popilli
XX	Aeb90828 Paenibaci
XX	Aa005680 btPgs1245
XX	Aa056922 Bacillus
XX	Aa041745 DNA encod
XX	Abk87234 Bacillus
XX	AdL15304 B. thuring
XX	Aeb45606 B. thurin
XX	Aeb34684 Bacillus
XX	Abk87235 Bacillus
XX	AdL15306 B. thuring
XX	Aeb45608 B. thurin
XX	Abk87247 Bacillus

PA (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX WPI: 2004-635574/61.
DR P-PSDB: ADR89406.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing Lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX Claim 1: SEQ ID NO 17; 178bp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 1686 BP; 624 A; 268 C; 348 G; 446 T; 0 U; 0 Other;
Query Match 100.0%; Score 1686; DB 13; Length 1686;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GAAATAGTCAAGGGCCATTCTTATAGATGTATGTAGTGAACAAATCTCAGAA 120
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DB 421 CGTTACGGGAAAGAAATTTGATGCTATCATGAAATGTTCCAAATGATTTGGCTATATGAG 480
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DB 481 CCTAATCCTTATGATGAGATTTATCGCTGTGATATCATGCTTCAAGTATGAGCCAAAGG 540
QY 541 TATCTTACACCAAGATGATATGCTCCGATATGATGATGATGATGATGATGATGAT 600
DB 541 TATCTTACACCAAGATGATATGCTCCGATATGATGATGATGATGATGATGATGAT 600

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DB 1141 CAACAAATGAGTAGAGCTTACGATTTAGTTCTATCAAAATGAGACGGGGGTATCTCA 1200
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 DB 1681 CCTTAA 1686

RESULT 2
 ID ADR89400 standard; cDNA; 5980 BP.
 XX ADR89400;
 AC
 XX 18-NOV-2004 (first entry)
 DT
 DE AXMI-008 full length coding sequence.
 XX
 XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX Bacillus thuringiensis.
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 FT /*tag= a
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 FT /transl_except= pos:168..170, aa:Met

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 XX 20-FEB-2004; 2004WO-US005829.
 PF
 XX 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.
 PR 20-FEB-2003; 2003US-0448806P.
 PR 20-FEB-2003; 2003US-0448810P.
 PR 20-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 XX
 XX (ATHE-) ATHENIX CORP.
 PA
 XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 PI
 XX WPI; 2004-635574/61.
 DR P-PsDB; ADR89402.
 XX
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX
 PS Claim 1; SEQ ID NO 12; 178bp; English.
 XX
 CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or

CC nucleic acids in products or organisms.
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 Query Match 100.0%; Score 1686; DB 13; Length 5980;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      3279 GTACCTTCTATGCGCGTCTGTAGCAATTTATATGATGTCACAAACCGATCCAAATAGG 3338
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Db      3339 CATGTAGGATATTTATATCAATGCCAGTTTCTCAGCCCTTCTTACACATCCCATCTTGT 3398
Oy      586  CCGCAAAATATATGATAGAAAGATGTAAGTGCAGATCCGATCCATTTGATTTTCAT 645
Db      3399 CAGGTAGCGCCCGGCAAAAACATGTGTATGTCAATTCATTCATCAATTCAGTTTCAT 3458
Oy      646  ATTGACACCGGAGAGATGATCAATATCAATATGAGTATGATGTCTTATTTAAAAAT 705
Db      3459 ATTGATAGGGGAGATGATTTACAAATCAAAATCAGAAATTTGGGTGTGTTTAAATC 3518
Oy      706  TCTAATCCAGATGATACGCTACAGTAGGGAATCTAGAAATCATTGAAAGAGACACTTA 765
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Oy      766  ACAGGTGAAGCATTTGGCAGATGTGAAACAAAAGAAAAGAAATGGAACACATGAGAG 825
Db      3579 AGAGCGGAAGCATGTACACATGTAAACAAAAGAAAAGAAATGGAATCAGCAAAATGAG 3638
Oy      826  AAAAAACGTGGGAAACACAACAAGCTATGATCCAGCAAAACAGGCTGTAGATGCATTA 885
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Oy      1126 GGAATGCCCGCGGTACAAACAATGATGAGCTTCAATTTAGTTCTATCAAAATGGAGC 1185
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Oy      1186 GCGGGGGTATCTCAAAACCTTGATGCTCAAGATCATGATGATGTGTAGTGTGAT 1245
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Oy      1486 ATGTATGACAAAGTTATATGAAATTTATATCAAAATCTAGGATGTATATACCA 1545
Db      4296 ATGTATGATCAAAAGTTATATGAGAAATTAATGTCAGAAATCTAGGATATGATATCA 4355
Oy      1546 GG 1547
Db      4356 GG 4357

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RESULT 4
ID      AAN82106
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XX
AC      AAN82106;
XX
DT      25-MAR-2003 (revised)
DT      31-OCT-2002 (revised)
DT      13-NOV-1990 (first entry)
XX
DE      Sequence contig. gene encoding Bacillus thuringiensis 8 protein.
XX
KW      Bt 8 protein; insecticides; mosquitoes; ss.
XX
OS      Bacillus thuringiensis.
XX
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FN      WO8806631-A.
XX
PD      07-SEP-1988.
XX
PF      03-MAR-1988; 88WO-US000734.
XX
PR      04-MAR-1987; 87US-00021405.
XX
PA      (UNMS ) UNIV MICHIGAN STATE.
PA      (PLAN-) PLANT GENETIC SYST.
PA      (UNMI ) UNIV MICHIGAN.
PI      Vaecck MA, Chungjatup W, McIntosh L;
XX
DR      WPI; 1988-271170/38.
XX
P      P-PSDB; AAP82314.
XX
PT      Chimeric gene for expression in Cyanobacteria - contig. DNA fragment
PT      coding for insecticidal active protein produced by Bacillus strain.
XX
PS      Disclosure; Page 7; 50pp; English.
XX
CC      This gene is ligated to a promoter region enabling expression in
CC      Cyanobacteria and the resultant chimeric gene is used to produce Bacillus
CC      thuringiensis 8 (Bt 8) protein. A truncated form of the protein can also
CC      be produced using a shorter gene. Transformed cyanobacteria and their
CC      progeny can be used in insecticidal compans., esp, for controlling
CC      mosquitos. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on
CC      25-MAR-2003 to correct PA field.)
XX
SQ      Sequence 3684 BP; 1302 A; 585 C; 693 G; 1103 T; 0 U; 1 Other:
Query Match      46.5%; Score 784.8; DB 1; Length 3684;
Best Local Similarity 72.3%; Pred. No. 1,3e-165;
Matches 1071; Conservative 0; Mismatches 387; Indels 24; Gaps 3;
Oy      1 GTGAGTCTTATGTTTACAGTAGTACGAAAAATACGTTTAAATAATGAAAACGACAGATTAT 60
Db      2113 GTGAATGACAGCTTTTACAAATGACCGGAAGATGATTTAAACATTGGAACGACAGATTAT 2172
Oy      61 GAAATGATCAAGCGCGCATTTCTATAGATGTATGATGATGAGCAAAATCCTCAGGAA 120
Db      2173 GACATAGATCAAGCGCGCAATCTTGTGAAATGATTTCTGAAAGATTTATTCACAAAAGAA 2232
Oy      121 AAAATATGTTATGAGATGAATAATAAAGCTGCAAAACAACTTATGTCAGTCTTGTATCTTA 180
Db      2233 AAAATGCTGTTATGATGAAAGTTAAATAATGCAAACTTATGTCATCTCGAAATGTA 2292

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QY 181 CTCGAAATGAGACTTT-----TCTGGAGATGATGGACATTCGGTATGATATATTC 234
D 2293 CTTGAAAAGGGGATTTTGAATCGGCTACGCTTGGTTGGAACAAGATGATATATCA 2352
QY 235 ATAGAGATCAATTAATCTTATTTTAAAGAAAATTTCTACAGATCGTGGAGCAGAGAC 294
D 2253 ATGAGAAAGATGATCTTATTTTAAAGGGCATTCCTTCATATGTCGGGCGAGAGAC 2412
QY 295 ATATATGGAATCTATTTCCAACTATATCTGTCAAAAAATAGATGATCTTAATTTAAA 354
D 2413 ATGATGATGATGATATTTCCAGCTATATTTCCAAAAATTTGATGATCAAAATTTAAA 2472
QY 355 CCATATACAGCTTATTCGAGTAAGAGGTTTGGGAGATGAAAGATTTGAAATTAATG 414
D 2473 CCGATACACCTTACTTATGTAAGGGATTTTGTAGAAATGTAAGATGTAGAACTAGTG 2532
QY 415 GTAAACGTTACGGGAAAAGAAATTTGATGATGATGATTTCCAAATGATTTGGCTAT 474
D 2533 GTTTCAGGCTATGGGGAAGAAATTTGATGATGATGATTTCCAGATTTTAACTAT 2592
QY 475 ATGAGAGCTTATCTTCAATGAGATTAATGCTGTGATATGATGCTCAGATGTAGC 534
D 2593 CTGATCTCTTCTAC-----CTTTGATGTGAAAGGCTTAATGTTGTAGAGC 2640
QY 535 CAAGGATCTCTACACCAAGATGATGATGCTCCGATATGATGATGATGATGATGATGAT 594
D 2641 TCCGCTGCGCGGCTTACATTTGGGAACCTTCTGATATGTTGATTTCACTCCAAATAT 2700
QY 595 ATAGATGAAAGATGTAAGTGTGACGATGCTCATTCATTTGATTTTCAATTTGACACC 654
D 2701 ACAGGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
QY 655 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
D 2761 GGGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
QY 715 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774
D 2821 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
QY 775 GCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
D 2881 GCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
QY 835 TGGGAAACACAACAAGCTTATGATCCAGCAAAACAGGCTGATGATGATGATGATGAT 894
D 2941 TCGGAAACACAACAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
QY 895 GAACAAGA-----GTTACATCATATTTACTTATGATGATGATGATGATGATGATGAT 948
D 3001 GTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
QY 949 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
D 3061 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
QY 1009 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
D 3121 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
QY 1069 CGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
D 3181 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
QY 1129 AATGCGGCGGTACACAACAATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
D 3241 AATGCGGCGGTACACAACAATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
QY 1189 GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1248
D 3301 GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
QY 1249 AAAAAAGAGAGCTGAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1308

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D 3361 AAAAAAGAGAGCTGAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
QY 1309 ACATTTAGTTCACTTTCTTGGGAAAGAGATATATGCAAAACAGATGATGATTTCCCA 1368
D 3421 AAATTTAGCTTTTACGTTTGTGAAAGAGATATATTTACGAAGACATGATGATTTCCCA 3480
QY 1369 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
D 3481 GATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
QY 1429 ATCGAGTTGCTTTGTATGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 1470
D 3541 ATGATTTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3582

RESULT 5
ABK14949
ID ABK14949 standard; DNA; 3684 BP.
XX
AC ABK14949;
XX
DT 29-AUG-2003 (revised)
DT 08-MAY-2002 (first entry)
XX
DE Bacillus thuringiensis variant israelensis toxin (Bt) gene sequence.
XX
KM Toxin; Bt; insecticidal; cyanobacterium; synechocystis 680; endotoxin;
XX mosquito control; glutamine synthetase inhibitor; inoculum; gene; ds.
OS Bacillus thuringiensis serovar israelensis.
XX
FH Key
FT RBS
FT 145..149
FT /*tag= a
FT /standard_name= "Shine-Dalgarno (SD) Sequence"
FT /note= "Consensus ribosome binding site"
FT 157..3567
FT /*tag= b
FT /product= "Bacillus thuringiensis toxin (Bt) protein"
FT /tranyl_except= (pos:1708..1710, aa:Ser)
FT /tranyl_except= (pos:2356..2358, aa:Gln)
FT /tranyl_except= (pos:3067..3069, aa:Gln)
XX
XX
XX US6335008-B1.
XX
XX 01-JAN-2002.
XX
XX 18-FEB-1992; 92US-00837625.
XX
XX 04-MAR-1987; 87US-00021405.
XX
XX 13-SEP-1988; 88US-00243798.
XX
XX (UNMS ) UNIV MICHIGAN STATE.
PI
PI Vaack MA, Chungjatupornchai W, McIntosh L;
XX
XX WPI; 2002-163196/21.
XX
XX P-PSDB; AAU76029.
XX
XX Novel chimeric gene expressed in cells of Cyanobacterium for controlling
XX mosquitoes in water, comprises a DNA fragment comprising promoter region
XX and a DNA fragment containing gene encoding for insecticidal protein.
XX
XX Example 2; Fig 2a; 36p; English.
XX
XX The present invention relates to a new chimeric gene expressed in cells
XX of a Cyanobacterium such as Synechocystis 680. The gene comprises a DNA
XX fragment having a promoter region, for expression of a DNA fragment in
XX the Cyanobacterium, and a fragment coding for an insecticidally active
XX protein endotoxin produced by Bacillus thuringiensis, B. sphaericus or B.
XX kurstaki strain, or for a truncated form of the protein. Cyanobacterium
XX is useful for controlling mosquitoes in water by applying the bacterium

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to a region to be controlled, where the cyanobacterium which contain and express the bar gene are selectively protected against competing non-transformed Cyanobacteria by treating the region with glutamine synthetase inhibitors. The invention is useful as viable inoculum to settle the region, especially the swamps and all stagnant waters which promote the growth of mosquito larvae. Cyanobacterium provides better control of mosquitoes, ensures a long-term destruction of mosquitoes, guarantees direct uptake of the bacterium by the mosquitoes and assures more stable availability of the toxin in the vicinity surface since it is self replicating and floats at or near the water surface. The present nucleic acid sequence encodes the B. thuringiensis variant israelensis toxin (Bt8) protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 3684 BP; 1301 A; 587 C; 694 G; 1102 T; 0 U; 0 Other;

Query Match 46.5%; Score 783.2; DB 6; Length 3684;

Best Local Similarity 72.2%; Pred. No. 2,9e-165;

Matches 1070; Conservative 0; Mismatches 388; Indels 24; Gaps 3;

```
QY 1 GTGAGTCTATGTTTAAAGTAGTACGAAAAATACGTTAAAAATAGAAAGACAGATTAT 60
DB 2113 GTGAATGCACTGTTTAAACAATACGCGAAAGATGCACTTAAACATTGGAAGACAGATTAT 2172
QY 61 GAAATAGATCAAGCGCCATTCTATAGAAATGATGTCAGATGAAACAAATCCTCAGAA 120
DB 2173 GACATAGATCAAGCGCAATCTTGAGAAATGATTTCTGAAGAAATTAATCCAAAAGAA 2232
QY 121 AAAATATGTTATGGATGAAATTAATACTGGCAAAACAATTAGTCAGTCTGTAATCTTA 180
DB 2233 AAAATGCTGTTTATAGATTAAGTAAAAATGCGAAACCACTTAGTCAATCTGAAATGTA 2292
QY 181 CTCCAAAATGAGACTT-----TCTGGAAATGATGAGCAATTCGATATGATATATTC 234
DB 2283 CTTCAAAAAGGGGATTTTGAATCGGCTACGCTTGTTGAGCAACAAGTATATATACACA 2352
QY 235 ATAGATGCAATATCTTATTTTAAAGGAAATTTCTACAGATGGTGGAGACAGAGC 294
DB 2353 ATTTGAAAGAGATGATCTTATTTTAAAGGCAATTCCTTCATATGCTGGGCGAGAGAC 2412
QY 285 ATATATGGAACCTCTATTTTCAACCTATCTGTCAAAAATATAGATGATCTAAATTAATA 354
DB 2413 ATTTGATGATGATATTTTCCGACCTATATATTCGAAAAATGATGAAATCAAAATTAATA 2472
QY 355 CCAATATACAGTTATCGAGTAAAGGGTTTGGGGAAGTAAAGTAAAGTAAATTAATG 414
DB 2473 CCGTATACAGTTACTAGTAAAGGGGATTTGTAAGGAAGTAAAGTAAAGTAAAGTAAAGT 2532
QY 415 GTTACACGTTACGGGAAAGAAATTTGATGCTATCAATGATTTCCAAATGATTTGGCTAT 474
DB 2533 GTTTACAGCTATAGGGGAAAGAAATTTGATGCTATCAATGATTTCCAAATGATTTGGCTAT 2592
QY 475 ATGACAGCTAATCTTTATGATGGAATATTCGCTGGAATTCATCGTCAATGATGAGC 534
DB 2593 CTGTATCTTTTAC-----CTTTGATTTGGAAGGCTTATATGCTGTGTAGAGC 2640
QY 535 CAAGGATCTTACCAACCAAGATGATATGCTCCGATATGATGATGATGATGATGATGAT 594
DB 2641 TCCGCTGTCGGCTTAAACATTTGGGAACACTTCTGATATGTTGATTTATGATGATGAT 2700
QY 595 ATAGATGAAAGATGTAAGTGTACGATCGTATCTTATGATTTTCAATTTGACAC 654
DB 2701 AAGGGAAGAAAGCAATGCTATGTCAGATTCCTCAATCAATTAATTTCAATTTGATGAT 2760
QY 655 GGAGAAAGTATACAAATGATGATTTGATGCTTTTAAATTTCTAATTTCA 714
DB 2761 GGGGCAATTAGTACAAATGATGATTTGATGCTTTTAAATTTCTAATTTCA 2820
QY 715 GATGATACGTTACAGTATGAGGAAATCTAGAATCTATTGAAGAAAGACCACTAAACGGTGA 774
DB 2821 GATGATACGTTACATTAATTAATTTGAAGTAAATTTGAAGAAAGGCAATTAATGATGGGAA 2880
QY 775 GATTGGGCAATGTGAAACAAAAGAAAGAAATGGAACACACATGAGAAAAAAGCT 834
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DB 2881 GCACTGTACGGGTGAACACATGGAGAAAGAAATGGAACGATCAAAATGAGCAAAACGT 2940
QY 835 TGGGAACACAAACAAGCCATGATCCAGCAAAACAGCGTGTAGATGATCATTTATTCAAAT 894
DB 2941 TGGGAACACAAACAAGCCATGATGATGAGAAACAAAGCCATGATGATGATTCACAAAT 3000
QY 895 GAACAGA-----GTACACTATCATATTTACTTTAGATCATATTTCAAAACGCTGATCA 948
DB 3001 GTACAAAGATGAGCGCTTACAGTTTATGCACTCGCTCAAAATTCAGATGCTGAGTAT 3060
QY 949 CTGTGACATGATTTCCCATATGATATACATATTTGTTACGAAAGCTCAGATGAAAC 1008
DB 3061 TTGTATACATGATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
QY 1009 TATGATGATATCAAGATGTAACAGCATGATGATGATGATGATGATGATGATGATGAT 1068
DB 3121 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
QY 1069 CGAAATGTCATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
DB 3181 AGAAATATTTATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
QY 1129 AATGCGGGGTCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
DB 3241 AATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
QY 1189 GGGGTATCTCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1248
DB 3301 GGGGTATCTCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
QY 1249 AAAAAAGAGACCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1308
DB 3361 AAAAAAGAGACCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 3420
QY 1309 AACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1368
DB 3421 AATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
QY 1369 GAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
DB 3481 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
QY 1429 ATGAGTTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
DB 3541 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3582
```

RESULT 6
AEA61392
ID AEA61392 standard; DNA; 3684 BP.
XX
XX AEA61392;
DT 11-AUG-2005 (first entry)
DE Bacillus thuringiensis Cry4Ba coding sequence, SEQ ID 2.
XX
XX Insecticide; cryetal protein; Cry4Ba; gene; ds.
XX
XX Bacillus thuringiensis.
OS
XX
XX Key Location/Qualifiers
FH 157.3567
FT /tag= a
FT /product= "Cry4Ba"
XX
XX US2005124803-A1.
XX
XX 09-JUN-2005.
XX
XX 30-AUG-2004; 2004US-00929754.
XX

PR 29-AUG-2003; 2003US-0498826P.
XX (OHIS) UNIV OHIO STATE RES FOUND.
XX Dean DH, Abdullah MA;
XX WPI; 2005-417057/42.
DR P-PSDB; AEA61391.
DR EMBL; X07423.
XX
PT New modified *Bacillus thuringiensis* insecticidal crystal proteins (i.e.
PT Cry4Ba and Cry19a) with enhanced toxicity, useful for reducing or
PT eliminating populations of target insects (i.e. mosquitoes) that are
PT vectors of disease.
XX
PS Disclosure; SEQ ID NO 2; 63bp; English.
XX
CC The present invention relates to modified insecticidal *Bacillus*
CC *thuringiensis* crystal proteins Cry4Ba and Cry19a which have enhanced
CC toxicity against a variety of insects, e.g. mosquitoes and lepidoptera.
CC The modified proteins are useful for reducing or eliminating populations
CC of target insects that are vectors of disease, particularly mosquitoes.
CC The present sequence is the coding sequence for the wild-type Cry4Ba
CC protein, which can be modified as follows: the amino acid aspartic acid
CC at position 454 is substituted with, for example proline, glycine,
CC alanine or threonine, and at least two or more additional amino acids are
CC inserted after the substitution, where the amino acids inserted after the
CC substituted amino acid at position 454 are selected from the combinations
CC of alanine and threonine or alanine and valine. In addition, the modified
CC Cry4Ba protein may comprise the following substitutions: Thr456 is
CC replaced with Ala; Asn578 is replaced with alanine; Thr456 is
CC with alanine; Ile580 is replaced with alanine; Asn579 is replaced with
CC Ile581 is replaced with alanine or phenylalanine.
XX
SQ Sequence 3684 BP; 1302 A; 587 C; 692 G; 1103 T; 0 U; 0 Other;
Query Match 46.5%; Score 783.2; DB 14; Length 3684;
Best Local Similarity 72.2%; Pred. No.2.9e-165;
Matches 1070; Conservative 0; Mismatches 388; Indels 24; Gaps 3;
QY 1 GTGAGTCTATGTTTACAAAGTAGTACGAAATAATCGTTAAATAATGAAACGACAGATTAT 60
DB 2113 GTGATGACACTGTTTACAAATGACCGGAAAGATGATTAAACATTGGAACGACAGATTAT 2172
QY 61 GAAATAGTCAAGCGCCATTCTATAGATGATAGTGAATGAAATCTCCAGAA 120
DB 2173 GACATAGTCAAGCGGCAAACTTGTGAATGATATTTCTGAAGAAATTAATCCAAAGAA 2232
QY 121 AAAATTAATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 2233 AAAATGCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2292
QY 181 CTCGAAAATGAGACTTT-----TCTGGGAATGATGACATTCGTTAATGATTAATC 234
DB 2293 CTTCAAAAACGGGGATTTTGAATCGGCTACGCTGGTTGACAAACAAAGATTAATATCA 2352
QY 235 ATAGAGTCCATTAATCCATTTTAAAGGAAATTTTCAAGATCCGCGGACGACGAAAC 294
DB 2353 ATTCAGGAAGATGATCTTAATTTTAAAGGCAATTAATCTTCATATGTCTGGGGCGAGAAC 2412
QY 295 ATATATGGAATCTATTTCCAACTATATCTGTCAAAAATAATGATGATGATGATGATGATGAT 354
DB 2413 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2472
QY 355 CCATATATACGTTATCGAGTAAAGGGTTTGTGGAGATGATGATGATGATGATGATGATGATGAT 414
DB 2473 CCGTATACACGTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2532
QY 415 GTACAGCTTACGGGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474
DB 2533 GTTTCACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2592
QY 475 ATGACAGCTTAATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534

DB 2593 CTGATCTCTTCTAC-----CTTGATGTGAGAGGCTCAATTCGTTGAGACG 2640
QY 535 CAAGGATATCTTACACCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
DB 2641 TCCGCTGTGCGGCTTAACATTTGGGAAACATTCGATATGTTGTTATGATGATGATGATGATGAT 2700
QY 595 ATGATATGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
DB 2701 ACAGGAAAGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
QY 655 GGAAGAT 714
DB 2761 GGGCATTTAGATTAACAAATGAAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
QY 715 GATGATATCGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774
DB 2821 GATGATATACGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
QY 775 GCATTTGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
DB 2881 GCATGAT 2940
QY 835 TGGGAAACACAAACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
DB 2941 TCGGAAACACAAACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
QY 895 GAACAAAG-----GTACATCATATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 948
DB 3001 GTACAAAGTGAAGCTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
QY 949 CTGAT 1008
DB 3061 TTGAT 3120
QY 1009 TATGAT 1068
DB 3121 TATGAT 3180
QY 1069 CGAAATGCTATTAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
DB 3181 AGAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3240
QY 1129 AATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
DB 3241 AATGCAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
QY 1189 GGGGATCTCAAAACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1248
DB 3301 GCGGATCTCAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
QY 1249 AAAAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1308
DB 3361 AAAAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
QY 1309 ACATTAAGTCACTTCTTGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1368
DB 3421 AATTTGACGTTTACGTTCTTGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
QY 1369 GAAAGTATCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
DB 3481 GATACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
QY 1429 ATGAGTTCCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
DB 3541 ATTTGAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3582
RESULT 7
ID AAN92515 standard; DNA; 4065 BP.
XX AAN92515;
AC AAN92515;

XX 25-MAR-2003 (revised)
DT 23-DEC-1990 (revised)
DT 15-MAY-1990 (first entry)
XX Sequence of insecticide gene from *Bacillus thuringiensis israelensis*
DE strain.
XX Insecticide; diptera larvae; aedes; ss.
XX
XX *Bacillus thuringiensis*.
OS
XX Key Location/Qualifiers
FH CDS 461..3868
FT /*tag= a
XX JP01080294-A.
XX
XX 27-MAR-1989.
PD
XX 21-SEP-1987; 87JP-00238394.
PF
XX 21-SEP-1987; 87JP-00238394.
PR
XX (SUMO) SUMITOMO CHEM IND KK.
PA (MARU-) MARUBENT KK.
XX
XX WPI; 1989-134798/18.
DR P-PSDB; AAP93308.
DR
XX Insecticide protein gene - from *Bacillus thuringiensis israelensis*
PT strain, used to produce protein toxic to diptera larvae, eg. aedes.
XX Fig 2; Fig 2-1 to 2-3; 8pp; Japanese.
XX
XX The protein gene has high insecticide activity to diptera larvae such as
CC aedes. (Updated on 25-MAR-2003 to correct PA field.)
CC
XX Sequence 4065 bp; 1471 A; 595 C; 752 G; 1247 T; 0 U; 0 Other:
SO
Query Match 46.5%; Score 783.2; DB 1; Length 4065;
Best Local Similarity 68.1%; Pred. No. 3e-165;
Matches 1161; Conservative 0; Mismatches 513; Indels 30; Gaps 4;
QY 1 GTGACTCTATGTTTACAAAGTAGTACGAAAAATACGTTAAATAAATGAAACGACAGATTAT 60
DB 2294 GTGAATGACACTGTTTACAAATGACGCGAAAGATGATTAAACATTGGAACGACAGATTAT 2353
QY 61 GAAATAGTCAAGCGCCATTCTATAGAAATGATGTCAGATGAACAAATTCCTCAGAA 120
DB 2354 GACATAGATCAAGCGCAAAATCTGTGGAATGATTTCTGAAGAAATTAATCAAAAGAA 2413
QY 121 AAAATAAATGTTATGGAATGAATAAATCTGCAAAACAACTTACGCTCGTATCTA 180
DB 2414 AAAATGCTGTTATTAAGATGAATTAATAATGCGAAACAACTTACGCTCGTATCTA 2473
QY 181 CTCGAAAAATGAGACTTT-----TCGGAATGATGAGCACTTCGTAATGATATATC 234
DB 2474 CTTCAAAAGCGGGATTTTGAATCGGCTACGCTTGATGGAACAAGATGATATATCA 2533
QY 225 ATAGATCCAAATATCTTATTTTAAAGAAATTTCTACAGATGCGTGGAGACAGAC 294
DB 2534 ATTCAAGAGATGATCTATTTTAAAGGCAATTAACCTTCATATGCTGGGCGAGAGAC 2593
QY 295 ATATATGGAATCTATTTTCAACCTATATCTGCAAAAAATAGATGATCTAAATTTAAA 354
DB 2594 ATTGATGATGATATTTTCCGACCTATATCTCAAAAAATGATGAATCAAAAAATTTAAA 2653
QY 355 CCATATACAGCTTATCGAGTAAAGGGTTTGTGGAAAGTAAAGTAAAGTAAATTAATG 414
DB 2654 CCGTATACAGCTTATCGAGTAAAGGGATTTGTAGAAAGTAAAGTAAAGTAAAGTAAAGT 2713
QY 415 GTAAACGCTTACGGGAAAGAAATGATGCTATCAAGAAATGTTCCAAATGATTTGGCCTAT 474

DB 2714 GTTTCACGCTATGGGGAAGAAATGATGCCATCATGATGATGTTCCAGCGATTTAAAGTAT 2773
QY 475 ATGACGCTTAATCCTTACATGAGAGATTATGCGTGTGAATATGCTCTCAGTATGTGAC 534
DB 2774 CTGATCCTTCTACCTTTGAT-----TGTAAGGGGTCTAAATCGTTGTGAGACG 2821
QY 535 CAAGGATTCCTTACCAACAGATGATGATGCTCCGATATGATATGATGATGCCGCAANT 594
DB 2822 TCCGTGTGCGGGCTTAACATTGGGAACACTCTGTGATATGTTGATTCATGCAATATGAT 2881
QY 595 ATAGATGAAGAGATGTAAGTGTGACAGATGTCATTCATTTGATTTTCAATATGACAC 654
DB 2882 ACAGGAAAAAGCATGCTGATGTCAGATATCCATCAATTTAGTTTCACTATGATATCA 2941
QY 655 GAGAGAGTATACAAATTAACAATGTAAGTATGATGCTTATTTAAATTTCTAATCCA 714
DB 2942 GGGGCTATGATATCAAAATGAATAATAGGGGTTGGGTCATGTTTAAATATCTTCTCCA 3001
QY 715 GATGATACGCTTACAGTATGGAATCTAGAACTCATGTAAGAAAGCACTAACAGGTGA 774
DB 3002 GATGATACGCTTACAGTATGGAATTTAGAACTTAATGAAAGAGGCCAATGATGGGAA 3061
QY 775 GCATTGCAACATGTGAACAAAGAAAGAAATGAAACAAACATGAGAGAAAAAGT 834
DB 3062 GATGATACGCTTACAGTATGGAATTTAGAACTTAATGAAAGAGGCCAATGATGGGAA 3121
QY 835 TGGGAACACAAAGCCTATGATTCAGCAAAACAGCGTGTATGATCATTTATTAAT 894
DB 3122 TCGGAACACAAAGCATATGATGTAGCGAAACAGCCATGATGCTTATTTCAAAAT 3181
QY 895 GAACAGAG-----TTACATATCATTTTCTTATGATCATTTCAAAAGCGTATGA 948
DB 3182 GTACAGATGAGGCTTACAGTGTGATGACACACTCGCTCAAAATCACTAGCGTATGAT 3241
QY 949 CTGATACAGTGAATTCCTATGATATACCATATTTGTTACGAAATGCTCCAGATATGAAC 1008
DB 3242 TTGTCATATGATTTCCATATGTGTGATGATGATGTTGTGATGATGATGAT 3301
QY 1009 TATGATGATATCAAGATTAACGACGATCATGCAAGGTTATTAATTTATGATGCA 1068
DB 3302 TATGATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3361
QY 1069 CGAAATGCTATTAACAAATGATGATCTTTCACAAAGATTAACAGGATGTCACGCAACAGA 1128
DB 3362 AGAAATATTTAAATAAGTATGATTTTACAAAGGGTAAATGGGTCATGATTAAGTGA 3421
QY 1129 AATGCGCGGTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
DB 3422 AATGCAAGCTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3481
QY 1189 GGGGATATCAAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1248
DB 3482 GGGGATATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3541
QY 1249 AAAAAAGAGAGCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1308
DB 3542 AAAAAAGAGAGCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3601
QY 1309 ACATTAAGTTCATCTTTCGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1368
DB 3602 AATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3661
QY 1369 GAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
DB 3662 GATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3721
QY 1429 ATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1488
DB 3722 ATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3781
QY 1489 TATGAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1548

Db 3782 GGAGAAAGTTTCTTCATGTTTAAATTCGATTTATTATTCGTGACAAAAATA 3841
Qy 1549 TATACAAACAATCTAATACCAAGACTCTG-----TAATATGATATATCAAAATTAATCT 1602
Db 3842 TATGAAAAACATAAAAAATATATCTAGAGACATAAAATTTATACAAATATCAATTC 3901
Qy 1603 AACATGATGACCTGATCTTCGGTTCGACATGTAAACCAAGGACATACCTGGCTGTACA 1662
Db 3902 ATTGATATGAAACGTTTATCCAAATATATATATATCCATTTAACTATCCAAACTCAAT 3961
Qy 1663 TGTATCAAGATATATACCGTTAA 1686
Db 3962 TGTATCAAGTATATGATGATTA 3985

RESULT 8
AAN91003
ID AAN91003 standard; DNA; 3535 BP.
XX
AC AAN91003;
XX
AC AAN91003;
XX
DT 25-MAR-2003 (revised)
DT 27-JAN-1991 (first entry)
XX
XX Sequence of toxin gene derived from a *Bacillus thuringiensis* var.
DE *israeliensis* (B.c.i.) microbe identified as strain HD567.
XX
XX Insecticide; diptera; mosquito; ss.
XX
OS *Bacillus thuringiensis*.
XX
FH Key Location/Qualifiers
FT CDS 1..3411
FT /*tag= a
XX
XX EP308199-A.
XX
PD 22-MAR-1989.
XX
PF 14-SEP-1988; 88EP-00308498.
XX
PR 18-SEP-1987; 87US-00098359.
PR 16-JUN-1988; 88US-00207690.
XX
XX (MYCO) MYCOGEN CORP.
XX
XX Gillyroy TE;
XX
XX PI
XX
XX WPI: 1989-087579/12.
DR P-PSDB; AAP93341.
PT *Bacillus thuringiensis* toxin toxic to dipteran insects - produced by gene
PT isolated from *Bacillus thuringiensis* var. *israeliensis* strain.
XX
PS Claim 2; pp 7-10 ; 13pp; English.
XX
XX A toxin active against dipteran insects, having a specified aa sequence
CC or a mutant having the same protein secondary structure or, if the
CC structure is altered, having the same biological activity, is claimed.
CC Also claimed is a DNA molecule including a nucleotide sequence encoding
CC the aa sequence. The novel toxin gene is toxic to dipteran insects e.g.
CC mosquito. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
CC MAR-2003 to correct PA field.)
XX
SQ Sequence 3535 BP; 1247 A; 573 C; 666 G; 1049 T; 0 U; 0 Other;

Query Match 46.4%; Score 781.6; DB 1; Length 3535;
Best Local Similarity 72.1%; Pred. No. 6.6e-165;
Matches 1066; Conservative 0; Mismatches 389; Indels 24; Gaps 3;

Qy 1 GTGAGTCCTATGTTTACAAAGTAGTACGAAAAATACGTTAAATAAGAAACGACAGATTAT 60
Db 1957 GTGAATGCACTGTTTACAAATGACGCGAAAGATGCAATTAAACATTGGAAACAGAGATTAT 2016

Qy 61 GAAATAGTCAAGGCCATTCTATAGAAATGTATGTCAATGTAACAAAATCCTCAGGA 120
Db 2017 GACATAGATCAAGCGCAAAATCTGTGAAATGTAATTTCTGAAGAAATATATATCAAAAAGA 2076
Qy 121 AAATTAATGTTATGGATGAAATTAACCTGGCAAAACAATAGTCAAGTCTGTATCTA 180
Db 2077 AAATGCTGTTATAGTATGAAAGTTAAATAATCGAAACAACTTATCATCTCGAAATGTA 2136
Qy 181 CTCAAAAATGAGACTTT-----TCTGGAAATGATTGACATTCCGTAATGATATATTC 234
Db 2137 CTTCAAAACCGGGGATTTTGAATCCGCTACCGCTGGTGGACACACAGATGATTAATATCA 2196
Qy 235 ATAGGATCAATATATCTATTTTAAAGSAAATTTCTACAGATGCGGAGACGAGAC 294
Db 2197 ATTCAGAGAGATGATCTTATTTTAAAGGCAATTACTTCATATGTTCTGGGCGCAGAGAC 2256
Qy 295 ATATATGGAACCTCATTTTCCAACTATATCTGTCAAAAATAGATGAGTCAATTAATAA 354
Db 2257 ATGATGTACGATATTTCCGACCTATATATTCAAAATAATGATGATCAAAATTAATAA 2316
Qy 355 CCATATACAGTTATCGAGTACAGGGTTGTGGAAATGATGAAGATTGAATTATATG 414
Db 2317 CCGTATACAGTTTACTAGTACAGGGATTTGTAGGAATGATGAAGATGTAAGACTAGTG 2376
Qy 415 GTACAGGTTACGGGAAAGAAATTGATGCTATCATGAATGTCCAAATGATTTGGCCTAT 474
Db 2377 GTTTCACGCTATGGGAAAGAAATGATGCAATCATGATGATGTTCCAGCTGATTTAACTAT 2436
Qy 475 ATGACGCTAATCCTTCATGTGAGATATGATATGCTGTGAATCATGCTCATGATGTAGC 534
Db 2437 CTGATCTCTTCTAC-----CTTGATTTGTGAAGGCTTATATCGTTGTGAAGACG 2484
Qy 535 CAAGGATATCTTACCAACAAGATGATATGCTCCCATATGATATGATGCCGCAAAAT 594
Db 2485 TCCGCTGTGCGGCTTAACATTTGGGAACATTCATGATATGTTGATTCATGCAATATGAT 2544
Qy 595 ATTAGTGAAGAAACAATGAAATGTCAGATGTCATGCTCATTTGATTTTCAATTTGACACC 654
Db 2545 ACAGGAAAGAAACATGTGCTATGTCAGGATTTCCATATATTTAGTTTCACTATGATACCA 2604
Qy 655 GGAAGATAGTACCAATATACAAATGTAGTATGATCTCTTATTAATAATTTCTATATCCA 714
Db 2605 GGGGCAATTAATATCAAAATGAAATATAGGGTTTGGGTCAATGTTTAAATATCTTCCCA 2664
Qy 715 GATGATACCGCTACAGTAGGAATCTTAGAATCTTAGAAGACCACTAACAGTGA 774
Db 2665 GATGATACCGCATCATTAATTAATTTAGAGTAAATGAAAGGCGCAATGATAGGGGAA 2724
Qy 775 GCATTGGCAGATGGAACAAGAAAGAAATGGAATGGAACAACAACATGAGAAABAAACGT 834
Db 2725 GCATGTCACGCGGAAACATGGAAGAAAGAAATGGAACATCAATGGAAGCAAAACGT 2784
Qy 835 TGGGAAACACAACAAGCCTATGATCCAGAAAACAGGCTAGATGATTAATTTTACAAAT 894
Db 2785 TCGGAAACACAACAAGCATATGATGTAACGAACAAACCCATTAATGCTTTATTCACAAAT 2844
Qy 895 GAACAGAA-----GTTACATATCATATTAATCTTATGATCATATTTCAAAACGCTGATCGA 948
Db 2845 GTACAAAGATAGGCTTACAGTTTGAATACGACACTCCCTCAAAATTCAGTACGCTGATAT 2904
Qy 949 CTGTTACAGTCGATTCCTCTATGTAATCCATTAATTTGGTTACGGAATGCTCCAGGATGAC 1008
Db 2905 TTGGTACAAATCGATTCATATGTTGTAACAAATGATTTGTTGCAAGATGTTCCAGGATTAAT 2964
Qy 1009 TATGATGTATATCAAGATTAAACGACGATATCATGCAAGTTATTAATTTATATGATGCA 1068
Db 2965 TATGATGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3024
Qy 1069 CGAAATGTCAATCAAAATGTTGACTTTTACCAAGATTTACAGGATGCGACGCAACAGGA 1128
Db 3025 AGAAATATTTTAAATGTTGATTTTACCAAGGCGGTTATGGGTTGTCATGTAACTGGA 3084

Qy	1129	AATGCCGGGAGACAA	CAAAATGGATGGAGCTT	CAGATATAGTTCTAT	CAAAATGGAGCGC	1188
Db	3085	AATGACAGCGTACAA	CAAAATAGATGGTGTTC	TCTGATTTGGTTCAT	CTAAATTTGGAGTGCT	3144
Qy	1189	GGGGTATCTCAAAA	CTTGCGATGCTCAAGATCAT	CATATGGATATGTGTTA	CGTGTGATTTGCC	1248
Db	3145	GGCGTATCTCAAAA	ATGTCCATCTCCACATATAT	CATGGGTATGTCTTA	ACGTGTATTGGC	3204
Qy	1249	AAAAAAGAGGACCT	GGAAAAAGGGTATGTAA	CGATGATGATTTGTAA	TATGAGAACAGAA	1308
Db	3205	AAAAAAGAGGACCT	GGAAAAATGGGTATGTAC	CGCTTATGATGTGGAGAA	GAATCAAGAA	3264
Qy	1309	ACACTTAAGTTCACT	TTCTTGGGAAGAGATATAT	GACAAAAACATGTAGAGTAT	TCCCA	1368
Db	3265	AAATTTGACGTTTAC	GTCTTGTGGAAGAGATATAT	TTCGAAAGACATGTAGAT	TGTTCCCA	3324
Qy	1369	GAAATGATGTGTGTA	CGGATTTGAAATAGGAGAAA	CCGAAAGGTACCTTATAT	ATATGATAGC	1428
Db	3325	GATACAGATCGTGTAC	GAATTTAGATTAAGCCGAAA	CCGAAAGGTTCGTTTATAT	ATATGAAAGC	3384
Qy	1429	ATTCAGTTGCTTTGAT	GTCAAGATATATGATTAACA	CATATTAATAC		1470
Db	3385	ATTGATTTAATTTTGC	ATGAACGAGTGAATTAAT	TAATAAAATTAAC		3426

XX	RESULT 9
XX	AAN96139
XX	ID AAN96139 standard; DNA; 4184 BP.
XX	AAN96139;
XX	
DT	27-AUG-2003 (revised)
DT	25-MAR-2003 (revised)
DT	15-MAY-1990 (first entry)
XX	
DE	Bacillus thuringiensis israelis strain toxin.
XX	
KW	Bacillus thuringiensis, israelensis strain; toxin; diptera larvae; aedes.
XX	
OS	Bacillus thuringiensis; israelensis.
XX	
XX	Key Location/Qualifiers
FT	CDS 461..3867
FT	/*tag= a
FT	/product= "toxin"
XX	
XX	JP01080294-A.
XX	
XX	27-MAR-1989.
XX	
XX	21-SEP-1987; 87JP-00238394.
XX	
XX	21-SEP-1987; 87JP-00238394.
XX	
XX	(SUMO) SUMITOMO CHEM IND KK.
PA	(MARU-) MARUBENI KK.
XX	
XX	WPI: 1989-134793/18.
DR	P-PSDB; AAP93308.
XX	
XX	Insecticide protein gene - from Bacillus thuringiensis israelensis
PT	strain, used to produce protein toxic to diptera larvae, eg. aedes.
XX	
XX	Fig 2(1) - 2(3); pages 639-40; Bpp; Japanese.
XX	
CC	The gene is used to produce protein toxic to diptera larvae, e.g. aedes.
CC	(Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC	correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
CC	on 27-AUG-2003 to correct OS field.)
XX	
XX	Sequence 4184 BP; 1501 A; 627 C; 774 G; 1282 T; 0 U; 0 Other;
XX	
XX	Query Match 46.0%; Score 776; DB 1; Length 4184;

[illegible]

Db 4106 GGGCATFAGATACAAATGAAAAATATAGGGGTTGGGCTCATGTTTAAATATCTCCAG 4165
Qy 716 ATGATATACGCTACAGTAGGGAATCTAGAAGTCATTGAAAGAACCACTAACAGGTGAAG 775
Db 4166 ATGATATACGCTACATTAATTAATTAAGAAGTAATGAAGAGGCCAATATAGTGGGAAG 4225
Qy 776 CATTGGCAATGTGAAACAAAAGGAAAAGAAATGGAACACACATGAGAGAAAAACGTT 835
Db 4226 CACTGTACGGGTGAAACACATGAGAGAAAGAAATGGAACGATCAATATGGAAGCAAAACGTT 4285
Qy 836 GGGAAACACAAACCAAGCTATGATCCAGCAAAACAGGCTGTAGATCATTTATTTACAAATG 895
Db 4286 CGGAACACCAACACATATGATGAGGAAACAGCCATTTGATCTTATTTACAAATG 4345
Qy 896 AACAGAA-----GTTACATATCATATTACTTTAGATCATATTTCAAAACGCTGATCAG 949
Db 4346 TACAAGATGAGGCTTTACAGTTTGATACGACACTCGCTCAATTCAGTATCGGTGATTT 4405
Qy 950 TGGTACAGTCGATTCCTATGATATACATTAATGGTTACCGAATGCTCAGGTATGAAC 1009
Db 4406 TGGTACATTCATTCATATGATATGATCAATGATGGTTGTTCAGATGTTCCAGGTATGAAT 4465
Qy 1010 ATGATGATATCAAGAGTTTAAACGACGATATGCAAGGTTATTAATTTATATGATGAC 1069
Db 4466 ATGATATCTATGATGAGTTTGATGACAGAGTGCCACAAAGCGGTTATTTTATGATACAA 4525
Qy 1070 GAAATGTCATACAAATGGTGACTTTTACACAGATTAACAGGATGCGACGCAACAGAA 1129
Db 4526 GAAATATATTAATAAATGGTGAATTTTACACAGGGTATGGGATGCGATGTAATCTGAA 4585
Qy 1130 ATGCGCGGTACACAAATGATGAGCTTCAGTATTTAGTTTATCAAAATTTGACCGGG 1189
Db 4586 ATGCAAGCGTACAAATAGATGGTGTCTGTATGGTTCTATCTAATTTGAGTGGCTG 4645
Qy 1190 GGGTATCTCAAACTGATGCTCAAGATCATCATGATGATGTTAGCTGATGTCGA 1249
Db 4646 GCGTATCTCAAAATGCTCATCTCCACATATCATGCGTATGTTTACGTTATTTGCGCA 4705
Qy 1250 AAAAAGAGACCTGGAAGAGGATGTAACGATGATGATTTGTAATGGAAGACAGAA 1309
Db 4706 AAAAAGAGACCTGGAAGATGGGTATGTCAGCTTATGATTTGAGGAGATCAAGAA 4765
Qy 1310 CACTTAAGTCACTTCTTCCGAAGAGATATATGACAAAACAGTAGAGTATTCGCG 1369
Db 4766 AATTGACCTTTACGCTTGTGAAAGAGATATATTAACGAAGACAGTAGATGATTTCCAG 4825
Qy 1370 AAAGTACGTGTACGATTTGAATAAGAGAAACGAAGTACATTTTATATAGATGCA 1429
Db 4826 ATACGATCGTGTACGAATGATGAGGGAACGGAAGGTTGTTTATATCGAAAGCA 4885
Qy 1430 TCGAGTGTCTTTGTATGCAAGATATGATTAACATATATAC 1470
Db 4886 TTGAATTATTTGATGCAAGCAGATTAATAAAAAATATAC 4926

RESULT 11
AA081178
ID AA081178 standard; DNA; 3543 BP.
XX
AC AA081178;
XX
DT 25-MAR-2003 (rev1sed)
DT 12-AUG-1995 (first entry)
XX
DE B.c. toxin PS71M3 gene.
XX
KM Delta-endotoxin; crystal protein; biological control agent; Calliphoridae;
KM screw-worm; sheep blowfly; Lucillia; Phormia; Calliphora; insecticide;
OS pesticide; B.c.; 89.
XX
OS Bacillus thuringiensis.
XX
FN W09502694-A2.

XX
PD 26-JAN-1995.
XX
PF 13-JUL-1994; 94W0-US007902.
XX
PR 15-JUL-1993; 93US-00093199.
PA (MYCO) MYCOGEN CORP.
XX
PI Hickie LA, Payne J;
XX
DR WPI, 1995-067338/09.
XX
P-PBDB; AAR63078.
XX
PT Method for controlling Calliphoridae pests - specifically utilises
PT Bacillus thuringiensis isolates or toxins.
XX
PS Disclosure: Page 36-38; 50pp; English.
XX
CC A library was constructed from Bacillus thuringiensis PS71M3 total
CC cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in Escherichia
CC coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This
CC was sequenced (AA081178). A cured, acrycetaliferous B.c. host carrying
CC pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to
CC calliphorids. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 3543 BP; 1278 A; 566 C; 612 G; 1087 T; 0 U; 0 Other;
XX
Query Match 45.3%; Score 763.8; DB 2; Length 3543;
Best Local Similarity 71.9%; Pred. No. 6,4e-161;
Matches 1050; Conservative 0; Mismatches 387; Indels 24; Gaps 3;
Qy 2 TGAGTCTTATGTTTACAGATGATGAGAAATATGTTTAAATAGAAACACAGATTATG 61
Db 2090 TTAATACATTTTATGCAATCTTAATAAAACACTTTACAACTTACAGATTATG 2149
Qy 62 AAATGATCAAGCGGCTATTTCTATAGATGATGTCAGATGAAACAAATCTCGGAA 121
Db 2150 ACATGATCAAGCGGCAATCTTGTGATGATATTTCTGAAGATTAATATCAAAAGAA 2209
Qy 122 AAATATGTTTATGGAATAATTAACATGCAAAACAACTTATGATGCTGCTGTAATCTAC 181
Db 2210 AAATCTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2269
Qy 182 TCCAAATGAGACTT-----TCTGGAAATGATGACATTCGTTATGATATATCA 235
Db 2270 TTCAAAAGGGGATTTGATCGGCTACGCTTGTGGAACAAAGTATATATCA 2329
Qy 236 TAGATCCATATATCTATTTTAAAGGAAATTTCTACAGTGGCTGAGACAGAC 295
Db 2330 TTCAAGAGATGATCTTATTTTAAAGGCAATTAACCTTCAATATGCTGGGGGGAAGAA 2389
Qy 296 TATATGAACCTTATTTCAACCTTATCTGCAAAAAATAGATGCTAATTTAAAC 355
Db 2390 TTGATGTATCAATATTTCCGACTATATATTCCAAAAAATGATGATCAAAATTTAAAC 2449
Qy 356 CATATACAGTTATGATGATGAGAGGTTTGGGAAGTATGAAAGATTTGAATTAATG 415
Db 2450 CGTATACAGTTACTAGTAAAGGGATTTGTAGGAAGTATGAAAGATGAGAACTAGTGG 2509
Qy 416 TAAACGTTACGGGAAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATG 475
Db 2510 TTTTACGCTATGGGGAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2569
Qy 476 TGCAGCTTAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 535
Db 2570 TGTATCTTTTAC-----CTTGTATGATGATGATGATGATGATGATGATGATGATG 2617
Qy 536 AAGGATATCTTACACCAACAGATGATGATGATGATGATGATGATGATGATGATGATG 595
Db 2618 CCGGTGCGGCTTAACTATGGAACACCTTGTATGATGATGATGATGATGATGATGATGATG 2677
Qy 596 TAGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 655

Db	2678	CAGGGAAAAAGATGCGTATGTCAGGATTTCCCATCAATTAGTTTCACTATTGTATPACG	2737
Qy	656	GAGAAGTAGATACAAATACAAATGATGATTTGATGTCTTATTAATAATTTCTAATCCAG	715
Db	2738	GGGCAATTAGATACMAATGMAAATATAGGGGTTTGGGTCACTGTTTAAATATCTTCCAG	2797
Qy	716	ATGATACCGCTACAGTAGGGAAATCTAGAAAGTCATTTAGAAAGAGACCACTAACAGGTGAG	775
Db	2798	ATGGATACCGCATCATTTAGATTAATTTTAGAAGTAAATGGAAGAGGCCAATAGATGGGGAA	2857
Qy	776	CATTGGCAATGTGMAAACAAAAGMAAAGAAATGMAACAAACATGGAAGAAAAACGTT	835
Db	2858	CACGTGCACGCGTGAACAACATGGAGMAAATAATGAAACATAAATGGAAGCAAAACGTT	2917
Qy	836	GGGAAACACAAACAGCGCTATGATCCAGCAAAAACGGCTGTAGATCATTTATTTACAAATG	895
Db	2918	CGGAAACACAAACAGCATATGATGTAGCGAAACAAACCATTAATCTTTATTCACAAATG	2977
Qy	896	AAACAAG-----GTTACATATCATATTTACTTTAGATCATATTTCAAAACGCTGATGCAG	949
Db	2978	TACAAGATAGAGCGCTTTTACAGTTTGTATTCACACACTCGCTCAATTCAGATACCGTGAATTT	3033
Qy	950	TGGTACAGTCGATTTCCCTATGATATACAAATATTTGGTTACCGAATCCTCAGGTATGAATCT	1008
Db	3038	TGGTACAAATCGATTCATATGTGTACAAATGATTTGGTTGTGAGATTTCCAGGATTAAGAAAT	3097
Qy	1010	ATGATGATATATCAAGAGTTAAACGACAGATCATCATCAAGGTTATATTAATTTATGATGCAC	1068
Db	3098	ATGATATCTATGTATAGATTTGATATGCACAGATGGCACAAACCGGTTATTTGTATGATACAA	3157
Qy	1070	GAAATGTCATTAACAATGGTGAATTTTACCAAGATTAACAGGATGGCACGCAACAGGAA	1128
Db	3158	GAAATATTAATTAATAATGGTGAATTTTACCAAGGGGTAAATGGGCTGGCATGTAATCTGAA	3217
Qy	1130	ATGCCCGCGTAAACAATATGATGAGCTTCAGTATTTAGTTTATCAAAATTTGGAGCGGG	1188
Db	3218	ATGCAGACGCTACAAACAAATGATGGTGTCTGTATGTGTTCTATCTAAATGGAGTGTGTG	3277
Qy	1190	GGGTATCTCAAACTTGCATGCTCAAGATCATCATGATATGTGTTCAGTGTATGTCGA	1248
Db	3278	GGGTATCTCAAAATGTCTCATCTCCAACTATATCAATGAGGTATGTCTTAGAGTGTATTTGCCA	3337
Qy	1250	AAAAAGAAAGAGCTGGAAGAAAGGGTATGTAAACGATGATGGATTTGTAAATGAAAGCAGAAA	1309
Db	3338	AAAAAGAAAGAGCTGGAAGAAATGGGTATGTCAACGCTTATGGATTTGTAGAGAAATCAAGAAA	3397
Qy	1310	CACCTTAAGTCACTTCTTGGCGAAGAAAGATATATGACAAAAACAGTAGAGTATTTCCAG	1368
Db	3398	AAATTACGTTTACGCTTGTGTGAAGAGGATATATTAACAAGACAGTAAATGATATTTCCAG	3457
Qy	1370	AAAGTATCGTGTACGGAATTTGAATATAGAGAAACGGAAGGTATCATTTTATATATGATACCA	1428
Db	3458	ATACAGATCGTGTACGAATTTGATAGATAGCGGAAACGGAAGGTTTCGTTTATATGAAAGCA	3517
Qy	1430	TCGAGTTGCTTTGTATGCAG 1450	
Db	3518	TTGAATTAATTTGCATGAACG 3538	
RESULT 12			
AAQ14669			
ID	AAQ14669	standard; DNA; 3543 BP.	
XX	AAQ14669;		
AC			
XX			
DT	27-AUG-2003	(revised)	
DT	25-MAR-2003	(revised)	
DT	04-FEB-1992	(first entry)	
XX			
DE	Dipteran active toxin gene.		
KM	Insecticide; B.t; crystal; delta endotoxin; cryIVA; sb.		

Db	2510	TTTCAAGCTTAATGGGAGAAATTGATGCCATCATATATGTTCCACTGATTTAACTATC	2568
Oy	476	TGCAGCCTTAATCTTTCATGTGGAGATTATCGCTGTGAATCAATCGCTCAGTATGAGCC	535
Db	2570	TGTATCTTTAC-----CTTTGATTGTGAAGGGCTTAATGTTGTGTGACGT	2617
Oy	536	AAGGTAATCTTACACCAACAGATGATATGCTCCGATATGTATGCATGCCGCAATA	595
Db	2618	CCGCTGTCCGGCTTAACATTTGGGAACACTTCTGATATGTGATTCATGCCAATATGATA	2677
Oy	596	TAGATAGAAAGCATGTGAAGTGTACGATTCGATCCATTTTGATTTTATATTTGACACG	655
Db	2678	CAGGGAAGAGATGTGCTATGTCCAGATTCCTCATCAATTTAGTTTCACTATGTATACG	2737
Oy	656	GAGAGTAGATACAAATACAAATGTAGTATTTGATGTCTTATTTAAAAATTTCTAATCCAG	715
Db	2738	GGGCACTTAGATACAAATGATAAAATATAGGGGTTTGGGTATGTTTAAAAATCTTCTCCAG	2799
Oy	716	ATGATATACGCTTACAGTAGGAATCTAGAAATCATTTGAAAGAGACCACTAACAGGTAG	775
Db	2798	ATGGATACGATCATTAAGTAAATTTAGAAATTTAGAAAGAGGCAATAGATGGGGAAG	2857
Oy	776	CATTGGCATGTGTGAACAAAAGAAAAAAGAAATGGAAACAACATGGAGAAAAACGTT	835
Db	2858	CAGTCTCACGCGTGAACACATGGAGAAAGAAATGGAAATGAAATGGAAGCAAAACGTT	2917
Oy	836	GGGAAACAACAACAGCCTATGATCCAGCAAAACAGCGTGTAGATCATTAATTTCAAAATG	895
Db	2918	CGAAAGACAACAACAGCATATGATGTAGGAAACAAGCCATTATATGCTTTATTCAAATG	2977
Oy	896	AACAAAG-----GTTACATCATATATTACTTTAGATCATATTTCAAAACGCTGATCAC	949
Db	2978	TACAGAATGAGGCTTTTACAGTTTGTATGAAACACATCGCTCAAAATTCAGTACCGTGTGATTT	3037
Oy	950	TGGTACAGTCCGATTCCTATGATATACCAATATGGTTACCGAATGCTCCAGGATGAGCT	1009
Db	3038	TGGTACATCGATTTCCATATGTATGTACAAATGATGGTGTGTGAGATTTCCAGGATGAATTT	3097
Oy	1010	ATGATGTATATCAAGAGTTTAAACGACCGATCATATGCAAGGTTATATTTATATGATGAC	1068
Db	3098	ATGACATCTATGTAGATGTGATGACGAGTGGCAACAAGCGGCTTATTTGATGATACAA	3157
Oy	1070	GAAATGTATTAACAATATGCTGACTTTTACACAAGATTACAGGATGCAACGACACAGAA	1128
Db	3158	GAAATATATTTAAAAATGTGTGATTTTACACAAGGGGTATGGGGTGCATGTATCTGGAA	3217
Oy	1130	ATGCCGGGTTCACAATAATGATGGAAGCTTCAATTTAGTTCTATCAAAATTTGAGCGGG	1189
Db	3218	ATGCAGACGTACACAATAATGATGATGTGTTCTGATATGTGTTCTATCTAATTTGAGATGCTG	3277
Oy	1190	GGGTATCTCAAAACCTTGCAATGCTCAAGATTCATCATGATATATGTGTTACGTGTATTGCA	1248
Db	3278	GCGTATCTCAAAATGTCCATCTCCAACATTAATCATGGGTAATGTCTTACGTGTATTGCA	3337
Oy	1250	AAAAAGAGAGCTTGGAAAAGGGTATGTATACATGATGATTTGTAATGAAAGCAGGAAA	1308
Db	3338	AAAAAGAGAGAGCTTGGAAAATGGGTATGTCAACGCTTATGATTTGTAGAGAGATCAAGAAA	3397
Oy	1310	CACCTTAAGTTCACCTTCTGCGAAGAAAGATATATGACAAAAACATAGAGGATATCCAG	1366
Db	3398	AATTCACGTTTACGTTCTTGTGAAGAAAGATATATTAACAGACATAGATGTATTTCCAG	3455
Oy	1370	AAAGTGAATCGTGTACGGAATGGAATATAGAGAAACGAAGGTACATTTTATATAGATAC	1428
Db	3458	ATACAGATCGTGTACGAATTTGATATAGGAGAAACGAAGGTTTCGTTTATATCGAAGCA	3517
Oy	1430	TCGAGTGTGTTGTATGCAAG	1460
Db	3518	TTGAATTAATTTGACATGAACG	3538

ID	AAN60055	standard; DNA; 10974 BP.
AC	AAN60055;	
XX		
XX		
DT	25-MAR-2003	(revised)
DT	07-JUL-1991	(first entry)
XX		
DE	VB131 clone circular plasmid from <i>Bacillus thuringiensis</i> var. israelensis encoding protein related to bacterial delta endotoxin.	
XX		
KW	Insecticide; microbial; ss.	
OS	<i>Bacillus thuringiensis</i> .	
XX		
FH	Key	Location/Qualifiers
FT	promoter	2833..2844 /*tag= a
FT	promoter	2854..2894 /*tag= b
FT	RBS	2904..2909 /*tag= c
FT	CDS	2916..6485 /*tag= d /product= "toxin" /note= "claimed DNA SQ"
FT		
PN	EP195285-A.	
XX		
PD	24-SEP-1986.	
XX		
PF	27-FEB-1986;	86EP-00102547.
XX		
PR	28-FEB-1985;	85US-00706836.
XX		
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.	
XX		
PI	Sekar VS, Carlton BD;	
XX		
DR	WPI; 1986-253299/39. P-PsDB; AAP60051.	
XX		
PT	Insecticidal protein related to bacterial delta-endotoxin - is obtd. by recombinant DNA methods from transform microorganism.	
PS	Disclosure; Fig 7; 69pp; English.	
XX		
CC	The patentors claim a toxic protein having an amino portion identical to the amino portion of delta-endotoxin from <i>Bacillus thuringiensis</i> var. israelensis and a carboxy-terminus portion different from the carboxy portion of the delta-endotoxin. The protein has the toxic properties of the delta-endotoxin. Appln. is at 0.2-10 x (10 to the 9) I.U./acre. (Updated on 25-MAR-2003 to correct PA field.)	
CC		
XX		
SQ	Sequence 10974 BP; 3554 A; 2038 C; 1772 G; 3610 T; 0 U; 0 Other;	
QY	Query Match	42.0%; Score 708.2; DB 1; Length 10974;
Db	Best Local Similarity	68.4%; Pred. No. 2.3e-148;
	Matches 1081; Conservative	0; Mismatches 466; Indels 32; Gaps 6
QY	1 GTGAGTCTATGTATTACAAGTAGTACGAAAAATAACGTTAAAAATGAAGAAGACAGATTAT	60
Db	4872 GTGAATGACACTGTATTACAAATGACCGAAGATGCATTAAACATTGGAACGACAGATTAT	4933
QY	61 GAAATAGATCAAGCGGCCATTTCATATAGAAATGTATGTACAGATGAACAAAATCCTCAGGA	120
Db	4932 GACATAGATCAAGCGCAAATCTTGTAAGTATTTCTGGAAGGAAATTATATCCAAAGAA	4993
QY	121 AAAATTAATGGTATGGATGAATAAATACTGGCAAAACAATTAGTCAGTCTGTAATCTA	180
Db	4992 AAAATGCTCTTATTTATGATGAAGTTAAAAATGCGAACAACATTAGCATCTTCGAAATGTA	5055
QY	181 CTCGAAAAATGGAGACTTT-----TCTGGGAATGATTGACATTCGGTAAATGATATTATC	234

Db	5052	CTTCAAAAGGGGATTTTGAAATCCGCTACGCTTGTTGAGACAAAGATGATATATTCACA	5111
Oy	235	ATAGATTCAAATTAATCCTATTTTTTAAAGAAAATTTCTACAGATCGGTGAGCAGAAC	294
Db	5112	ATTCAAGAAAGATGATCCTATTTTTTAAAGGCAATTACCTTCATATGTCGGGGCAGAGAC	5171
Oy	295	ATATATGGAACTATTTTCCAACTATATCTGTCAAAAAATAGATAGCTTAATTTAAA	354
Db	5172	ATTGATGTAGCATATTTTCCGACCTATATATTCAAAAAATTGAATGAAATCAAAATTTAAA	5231
Oy	355	CCATATACCGTTATCGAGTAAAGAGGGTTGGGGAAGATGAAAGATTTGAAATTTATG	414
Db	5232	CCGATACACGTTACTTACGTAAAGGGGATTTGAGGAAGATGAAAGATGAGAACTAGTG	5291
Oy	415	GTAAACAGCTTACGGGAAAGAAATTTATGCTATCATGAAATGTTCCAAATGATTTGGCTAT	474
Db	5292	GTTTCAACCTATAGGGGAAGAAATTTATGCCATCATGAATGTTCCAGCTGATTTAAACTAT	5351
Oy	475	ATGCAGCCTAATCCTTATGTTGAGATTAATGCTGTGAATCATCGTCTCAGTATGTAGC	534
Db	5352	CTGTATCCTTCTACCTTGAATGTGA-----AGGGCTAATCGTTGTAGC	5396
Oy	535	CAAGGATATCTTACACCAACAGATGATATGTCCTCCGATATGATATGATATGCCCGAAAT	594
Db	5397	GTCCCGTGTGCGCTACACATTTGGGACACTTGTATATGTTGATATTCATGCGCAATATGAT	5456
Oy	595	ATAGATGAAAGCATGTGAGTGTACAGATCGTCATCCATTTGATTTTATATTTACACAC	654
Db	5457	ACAGGAAAAAGCATGTGCTATGTATGATATCCATCATTTAGTTTCACTATTTGATATCA	5516
Oy	655	GGAGAGTAGATACAAATACAAATGTAGATATGATATGTTATTTAAAAATTTCTAATCA	714
Db	5517	GGGGCATTAGATACAAATGAAAAATATAGGGGTTGGGTCAATGTTAAATATCTTCTCA	5576
Oy	715	GATGATACGCTACAGTAGGGAATTTAGAAATGCTATGAAAGAGCACTAACAGGTGAA	774
Db	5577	GATGATATCGCATCTTATGATTAATTTAAGATTAATGAAAGGGCCAAATGATGGGGAA	5636
Oy	775	GCATTGGCACAATGTAAAACAAAAAGGAAAAATGGAACAAACATAGAGAAAAAGT	834
Db	5637	GCACTGTACACGGGTGTAACCAATGAGAGAAATGAAAGATCAATGAAAGCAAAAGCT	5686
Oy	835	TGGGAAACAAACAAGCCTATGATCAGCAAAAAGCGCTGATAGATCTTAATTTACAAT	894
Db	5697	TCGGAAAACAAACAAGCATATGATGTAGCGAAAACAAGCATTAATGCTTTATTCAAAT	5756
Oy	895	GAAACAAG-----GTACACTATATATTAATTTAGATCATATTTCAAAAGCGTGTATGA	948
Db	5757	GTACAAGATGAGGCTTTACAGTTGATATCGACACTCGCTCAAAATTCAGATAGCGCTGAGAT	5816
Oy	949	CTGGTACAGTCGATTCCTCATATGATATACATTAATTTGATACGAATGCTCCAGATGAAAC	1008
Db	5817	TTGGTACATGATTCATATATGTGTACATATGTTGTGTACAGATGTTCCAGATATGAT	5876
Oy	1009	TATGATGATATCAAGAGTTAAACGACGATATCATGCAAGGTTATTAATTTATATATGCA	1068
Db	5877	TATGATATCTATGTAGATGTGGATGCAAGATGGCAACAAGCGCTATTGTTGATGATACA	5936
Oy	1069	CGAAATGCTATPACAAATGTGTGACTTTACACAAGATTTACAGGATGGCAAGCAACAGA	1128
Db	5937	AGAAATATTAATTAATAAATGTTGATTTTACACAAGGGGTAAATGGGGGTGCATGTAACTGA	5996
Oy	1129	AATGCGCGGTGACAACAAAATGGAATGGACCTCAGATTAATGTTCTATCAAAATTTGAGCGCG	1188
Db	5997	AATGACAGCTPACAACAAAATGATGTGTGTTCTGTATGTGTTCTATCTPAAATTTGAGTGCT	6056
Oy	1189	GGGGATCTCAAACTTGCATGCTCAAAATCATCATGATATATGTTTACGTTGATTTGCC	1248
Db	6057	GGCGATCTCAAAATGTCCATCTCCAACTATATATATATGGTATATGTTTACGTTATTTGCC	6116
Oy	1249	AAAAAGAGAGCTGAAAAGGGTATGTAAAGATGATGATTTGTATG- GAAAGCAGGA	1307

Db	6117	AAAAAAGAGACCTGGAAATGGGTATGTACCGTTATGGATTGTGAGAGAAATCAAGA	61175
Oy	1308	AACACTTAAGTTCACCTTCTTGCGAAGAGATATATGACAAAAACAGTAGAGTATTC	1367
Db	6176	AAATATGACGTTTACGCTTGTTGMAAGAGATATATATACGAAGACAGTAAATGATTC	6235
Oy	1368	AGAAAGGATCGTGT---ACGGATTGAATATGAGAAACCGAAGGTACATTTATATAGA	1424
Db	6236	AGATACAGCAATTCGTGCACGAATATGGAATAGCGAAACCGAAGTTCTTTATATCGA	6295
Oy	1425	TAGCATGAGTGTGTTTGTTATGCAAGATATGATTAACATTAATTAAGTTCGACACGGGTAA	1484
Db	6296	AAGCATTTGAATTAATTTGCATGACAGACGTATTAATTAATAAAGTTATATTA	6355
Oy	1485	TATGTATGAGCAAGTATATATAGGAAATTAATTAATCAAAATACTAGCGATGTATTAACA	1544
Db	6356	ACACTGGAGAAAGTTTCTCCATCGTTTATTAATTTTCGATTTATTAATTTTCGTACAA	6415
Oy	1545	AGGCTATTCAAACACACTATTA	1565
Db	6416	AAATATATATGAAAAACATATA	6436
RESULT 14			
AAN93059			
ID	AAN93059	standard; DNA; 4571 BP.	
XX	AAN93059;		
AC			
XX			
AC	27-AUG-2003	(revised)	
DT	25-MAR-2003	(revised)	
DT	30-MAY-1990	(first entry)	
XX			
XX			
DE		Delta-endotoxin crystal protein gene.	
XX			
XX		Delta-endotoxin; crystal protein; insecticide; pch130; ss;	
KM		biological control agent.	
KM			
XX			
OS		Bacillus thuringiensis; israelensis.	
XX			
XX			
FH	Key	Location/Qualifiers	
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FT		/label= Shine-Dalgarno sequence.	
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FT		/*tag= a	
FT		/product= "delta-endotoxin crystal protein"	
XX			
PN	EP296870-A.		
XX			
XX			
PD	28-DEC-1988.		
XX			
PE	24-JUN-1988;	88EP-00305772.	
XX			
PR	26-JUN-1987;	87US-00067653.	
XX			
PA	(DUPO) DU PONT DE NEMOURS & CO E I.		
XX			
PI	Ellar DJ, Ward ES;		
XX			
XX	WPI; 1989-001322/01.		
DR	P-PSDB; AAP93715.		
XX			
PT		DNA fragment encoding insecticidal protein - obtd. from Bacillus	
PT		thuringiensis sub species israelensis, and used in microorganisms and	
XX		plant cells.	
XX			
PS	Disclosure; Fig 7; 26pp; English.		
XX			
CC	The sequence encodes the 130 kDa delta-endotoxin gene from B.		
CC	thuringiensis subsp. israelensis and is a 4.46 kb insert of pch130. The		
CC	delta endotoxin protein is insecticidal and can be used to control insect		
CC	pests esp. mosquitos. See also AAN93054. (Updated on 25-MAR-2003 to		

CC correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 4571 BP; 1678 A; 685 C; 817 G; 1391 T; 0 U; 0 Other;
 SQ Query Match 37.8%; Score 637.8; DB 1; Length 4571;
 Best Local Similarity 66.2%; Pred. No. 1,1e-133;
 Matches 1060; Conservative 0; Mismatches 397; Indels 144; Gaps 4;

2 TGAGTCTATGTTTACAGTAGTACGAAATAACGTTAAATAAGACGACAGATTATG 61
 Db TTAATACATTTTATGCAATCTTATPAAAAACATTTACATCAGAACCTTACAGATTATG 3039
 Qy 2980 TTAATACATTTTATGCAATCTTATPAAAAACATTTACATCAGAACCTTACAGATTATG 3039
 Db 62 AAATGATCAAGCGGCCATTTCTATAGAAATGATGTCAGATGACAAATAATCTCGAGAA 121
 Qy 3040 ACATAGATCAAGCGGCCAATCTTGGAATGATTTCTGAAAGATTATATCCAAAGAA 3099
 Db 122 AAATATGTTTATGGAATAAATACTGGCAAAACATTAGTCAAGTCTGTAATCTAC 181
 Qy 3100 AAATGCTTTTATGATGATGATTAATAATGCGAAACAACTTAGTCAATCTCGAAATGAC 3159
 Db 182 TCCAAATGAGACTTT-----TCTGGAAATGATTGACATTCGGTATGATATTATCA 235
 Qy 3160 TTCAAAAGGGGATTTGATCGCTACGCTTGTTGACAAACAGTATATATACAA 3219
 Db 236 TAGGATCCATATATCTTATTTTAAAGAAATTTCTACAGTCCGTGAGCAGACACA 295
 Qy 3220 TTCAAGAGATGATCTTATTTTAAAGGCAATACCTTATATGTCGTGGGGGAGAGACA 3279
 Db 296 TATATGGAAGCTTATTTCCAACTTATCTGTCGAAATAATGATAGTCTAATTAAC 355
 Qy 3280 TTGATGATGATATTTCCGACCTATATATTCGAAATAATGATATCAAAATTTAAAC 3339
 Db 356 CATATACAGTATTCGATTAAGAGGTTTGTGGAGATGATTAAGATTGAATTAATG 415
 Qy 3340 CGTATACAGTATTCGATTAAGAGGTTTGTAGAGATGATTAAGATTGAATTAATG 3399
 Db 416 TAAACGTTACGGGAAAGAAATTTGATGATGATGATGATGATGATGATGATGATGAT 475
 Qy 3400 TTTCAAGCTATGCGGAAATAATGATGATGATGATGATGATGATGATGATGATGATGAT 3459
 Db 476 TGCAGCTATTCCTCATGTGGAATTTACGCTGATGATGATGATGATGATGATGATGATGAT 535
 Qy 3460 TGTATCTTTTAC-----CTTGATTTGAAAGGCTTATATCTTGTGAGACGT 3507
 Db 536 AAGGATATCTTACCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
 Qy 3508 CCGCTGTCGGGCTTAACTTGGGAACACTTGTGATGATGATGATGATGATGATGATGATGAT 3567
 Db 596 TAGATGAAGCATGTGAAGTGTCAAGTCTCATCTTATTTTATTTATTTATTTATTTATTT 655
 Qy 3568 CAGGGAAGGATGCTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3627
 Db 656 GAGAGTGAATCAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715
 Qy 3628 GGGCTTGAATCAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3687
 Db 716 ATGATAGCTTACAGTAGGGAATCTAGAGT----- 746
 Qy 3688 ATGATAGCTTACAGTAGGGAATCTAGAGT----- 746
 Db 747 ----- 746
 Qy 3748 CACTGTACGCGTGAACAACATGAGAAAGAAATGGAACGATCAAAATGGAACAAACGTT 3807
 Db 747 -----CAATGAAGAGGACCACTTAAACAGTGAAG 775
 Qy 3808 CGGAAACACACACAGCATATGATGATGCGAAATTTGAAGAGGCGCAATAGATGGGAAAG 3867
 Db 776 CATTGGCACTATGTAACAAAGAAAGAAATGGAACACACATGAGAAAGAAACGTT 835
 Qy 3868 CACTGTACGCGTGAACAACATGAGAAAGAAATGGAACATCAAAATGGAAGCAAAACGTT 3927
 Db 836 GGGAAACACACACAGCATATGATCCAGCAAAACAGGCTGTAGATGATTTATTTACAAATG 895

Db 3928 CGGAAACACACACAGCATATGATGAGAAAGAAACAGCATGATGATGATTTATTTACAAATG 3987
 Qy 896 AACACAG-----TTACATATCATATTTACTTTAGATCATATTTCAAAACGCTGATGAC 949
 Db 3988 TACAAGATGAGGCTTTACAGTTTATGATGACACTGCTCAATTTACAGTACGTGATTT 4047
 Qy 950 TGTATCACTGATTTCCCTATGATATCCATATTTGTTACGAAATGCTCCAGTATGAAT 1009
 Db 4048 TGTATCACTGATTTCCCTATGATATCCATATTTGTTACGAAATGCTCCAGTATGAAT 4107
 Qy 1010 ATGATGATATCAAGATTTAAACGAGTATCATGACAAAGTTATTAATTTATATGATGAC 1069
 Db 4108 ATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4167
 Qy 1070 GAAATGATATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129
 Db 4168 GAAATGATATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4227
 Qy 1130 ATGCGCGGATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189
 Db 4228 ATGCGAGTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4287
 Qy 1190 GGGTATCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1249
 Db 4288 GGGTATCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4347
 Qy 1250 AAAAAGAGAGCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1309
 Db 4348 AAAAAGAGAGCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4407
 Qy 1310 CACTTAAGTCACTTTTTCGAGAGAGATATGACAAACAGTACAGGATTTCCAG 1369
 Db 4408 AATGACGTTTACGCTTGTGAAGAGATATATACAGAGCAGTATGATTTCCAG 4467
 Qy 1370 AAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1429
 Db 4468 ATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4527
 Qy 1430 TCGAGTCTTGTATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
 Db 4528 TTGATTTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4568

RESULT 15
 AAN93054
 ID AAN93054 standard; DNA; 3940 BP.
 AC AAN93054;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 30-MAY-1990 (first entry)
 XX
 DE Delta-endotoxin crystal protein gene.
 DE
 KW Delta-endotoxin; crystal protein; insecticide; sw; pcc130;
 KW biological control agent.
 XX
 OS Bacillus thuringiensis; israelensis.
 XX
 FH Key Location/Qualifiers
 FT RBS 879..884
 FT /*tag= b
 FT /*label= Shine-Delgarno sequence
 FT 891
 FT /*tag= a
 FT /product= "delta-endotoxin"
 PD 28-DEC-1988.
 XX

PF 24-JUN-1988; 88EP-00305772.
 XX 26-JUN-1987; 87US-00067653.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Eliar DJ, Ward ES;
 PI WPI; 1989-001322/01.
 DR P-PSDB; MAP94035.
 XX
 XX DNA fragment encoding insecticidal protein - obcd, from *Bacillus*
 PT *thuringiensis* sub species *israelensis*, and used in microorganisms and
 PT plant cells.
 PS Disclosure; Fig 5; 26pp; English.
 XX
 CC The nucleotide sequence is an insert in plasmid pCC130. The delta
 CC endotoxin protein is insecticidal and can be used to control insect pests
 CC esp. mosquitoes. See also AAN93059. (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)
 CC
 XX Sequence 3940 BP; 1457 A; 603 C; 659 G; 1221 T; 0 U; 0 Other;
 SQ
 Query Match 26.6%; Score 448.6; DB 1; Length 3940;
 Best Local Similarity 68.9%; Pred. No. 2.3e-90;
 Matches 670; Conservative 0; Mismatches 279; Indels 24; Gaps 3;
 QY 2 TGAGTCTTATGTTTCAAGTACGAAAAATACCTTAAATAGAAACGACATTTATG 61
 DB 2380 TTAATACATTTTATGCAAAATCTTATMAAAACACTTTCAAATCAGACTTATG 3039
 QY 62 AAATGATCAAGCGGCCCTTCTATAGATGATGTCAGATGAACAAATCCTCAGSAA 121
 DB 3040 ACATGATCAAGCGGCCCAATCTTGAGATGATTTCTGAAGAAATTATCCAAAGSAA 3099
 QY 122 AAATATGTTATGGGATGAATAAACTGCAAAACAACTTAGTCAGTCTGTAATCTAC 181
 DB 3100 AAATGCTGTTATTTAGTGAATGAAAAATGCAAAACAACTTAGTCAGTGAATGTA 3159
 QY 182 TCCAAAAATGAGACTT-----TCTGGGAATGATGGACATTCGGTAATGATTTATCA 235
 DB 3160 TTCAAAAAGGGGATTTGAAATCGGCTACGCTTGGTTGGACAAAGTATATATCAAA 3219
 QY 236 TAGATCCAAATTAATCTATTTTAAAGSAAATTTCTACAGATGCGTGAGACAGAGACA 295
 DB 3220 TTCAAGAAAGATGATCTATTTTAAAGGCAATTAACCTTCAATATGTCGGGCGAGAGACA 3279
 QY 296 TATATGGAATCTATTTTCAACTATATCTGTCAAAAAAATAGATGATCTAAATTAANAAC 355
 DB 3280 TTGATGGATGATATTTTCCGACTATATATTCAAAAAATGATGAATCAAAATTTAANAAC 3339
 QY 356 CATATACAGTTATCGAGTAAGAGGTTTGTGGGAAGTAGTAAAGATTGAATTTAATGG 415
 DB 3340 CGTATACACGTTACTAGTAAGGGAATTTGTAGGAAGTAGTAAGATGTAAGACTAGTGG 3399
 QY 416 TAAACGTTACGGGAAGAAATGATGCTATCATGAATGTCCAATGATTTGGCTATA 475
 DB 3400 TTTACGCTATGGGGAAGAAATGATGCTATCATGAATGTCACGCTGATTTAAACTATTC 3459
 QY 476 TGCAGCTTAATCTTCAATGTGAGATTATCGCTGTAATCATCGTCTCAGTATGAGCC 535
 DB 3460 TGTATCTTCACTTTGAT-----TGTGAAGGCTTAATGCTTGTGAGAGCT 3507
 QY 536 AAGGGTATCTTACACCAACAGATGATATGCTCCGATATGATGATGATGATGATGATG 595
 DB 3508 CCGCTGTGCGGCTTAACATTTGGGAACACTTGTGATGATGATGATGATGATGATGATG 3567
 QY 596 TAGATAGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 655
 DB 3568 CAGGGAAGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3627
 QY 656 GAGAAAGTAGATACAAATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 715

DB 3628 GGGCATTAGATACAAATGAAAAATATAGGGGTTTGGGTCAATGTTAAATATCTTCTCCAG 3687
 QY 716 ATGATACGCTTACATGATGGGAATCTAGAGTCAATTGAAGAGACCACTAACAGTGAAG 775
 DB 3688 ATGATACGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3747
 QY 776 CATTGGCAATGTGAACAAAGAAAGAAATGGAACCAACATGAGAGAAAAACGTT 835
 DB 3748 CACTGTCAAGGCTTAAACATGAGAGAAAGAAATGGAACCAATGAGAGAAAAACGTT 3807
 QY 836 GGAAGAACAAACAGCTTATGATCAGCAAAACAGGCTGATGATGATGATGATGATGATG 895
 DB 3808 CGGAAACAAACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3867
 QY 896 AACAAAG-----GTTACATATCATTTACTTTAGTCAATTTCAAAACGCTGATGAC 949
 DB 3868 TACAAAGTAGAGCTTTTACAGTTTGTATGACACACTCGCTCAATTCAGTACCGTGAATTT 3927
 QY 950 TGTACAGTGCAT 962
 DB 3928 TGGTACATGAT 3940

Search completed: February 15, 2006, 03:49:03
 Job time : 1069 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 03:49:14 ; Search time 1453 Seconds
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Title: US-10-781-979-6

Perfect score: 1686
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1686	100.0	5980	8 US-10-781-979-1	Sequence 1, Appl1
3	914.8	54.3	4391	9 US-10-929-754-4	Sequence 4, Appl1
4	783.2	46.5	3684	9 US-10-929-754-2	Sequence 2, Appl1
5	384.2	22.8	4359	5 US-10-120-544A-3	Sequence 3, Appl1
6	384.2	22.8	4359	5 US-11-091-654-3	Sequence 3, Appl1
7	379	22.5	3504	10 US-10-089-678-2	Sequence 2, Appl1
8	379	22.5	3590	5 US-10-089-678-3	Sequence 3, Appl1
9	313	18.6	4896	6 US-09-756-526A-3	Sequence 3, Appl1
10	313	18.6	4896	6 US-10-345-020-3	Sequence 3, Appl1
11	313	18.6	4896	6 US-10-342-821-3	Sequence 3, Appl1
12	312.8	18.6	4366	5 US-10-120-544A-19	Sequence 19, Appl1
13	312.8	18.6	4366	5 US-11-091-654-19	Sequence 19, Appl1
14	306.4	18.2	4359	5 US-10-120-544A-17	Sequence 17, Appl1
15	306.4	18.2	4359	10 US-11-091-654-17	Sequence 17, Appl1
16	302.6	17.9	3621	5 US-10-032-717-1	Sequence 1, Appl1
17	302.6	17.9	3621	5 US-10-414-637-1	Sequence 1, Appl1
18	302.6	17.9	3621	7 US-10-606-320-1	Sequence 1, Appl1
19	302.6	17.9	3621	8 US-10-746-914-1	Sequence 1, Appl1
20	302.6	17.9	3621	10 US-11-021-115-5	Sequence 5, Appl1
21	302.6	17.9	3633	6 US-10-032-717-3	Sequence 3, Appl1
22	302.6	17.9	3633	6 US-10-414-637-3	Sequence 3, Appl1
23	302.6	17.9	3633	7 US-10-606-320-3	Sequence 3, Appl1

24	302.6	17.9	3633	8 US-10-746-914-3	Sequence 3, Appl1
25	302.6	17.9	4874	5 US-10-032-717-27	Sequence 27, Appl1
26	302.6	17.9	4874	6 US-10-414-637-27	Sequence 27, Appl1
27	302.6	17.9	4874	7 US-10-606-320-17	Sequence 17, Appl1
28	302.6	17.9	4874	8 US-10-746-914-17	Sequence 17, Appl1
29	302.6	17.9	4874	8 US-10-032-717-28	Sequence 28, Appl1
30	302.6	17.9	6613	6 US-10-414-637-28	Sequence 28, Appl1
31	302.6	17.9	6613	7 US-10-606-320-18	Sequence 18, Appl1
32	302.6	17.9	6613	8 US-10-746-914-18	Sequence 18, Appl1
33	302.4	17.9	4188	5 US-10-120-544A-5	Sequence 5, Appl1
34	302.4	17.9	4188	10 US-11-091-654-5	Sequence 5, Appl1
35	299.2	17.7	6930	3 US-09-756-526A-1	Sequence 1, Appl1
36	299.2	17.7	6930	6 US-10-345-020-1	Sequence 1, Appl1
37	299.2	17.7	6930	6 US-10-342-821-1	Sequence 1, Appl1
38	275.2	16.3	3465	10 US-11-018-615-26	Sequence 26, Appl1
39	271.8	16.1	3507	7 US-10-614-524-3	Sequence 3, Appl1
40	269.6	16.0	3453	5 US-10-099-285-75	Sequence 75, Appl1
41	269	16.0	4344	9 US-10-687-879A-4	Sequence 4, Appl1
42	268.8	15.9	3471	5 US-10-099-285-73	Sequence 73, Appl1
43	268.8	15.9	3471	6 US-10-428-961-27	Sequence 27, Appl1
44	265.8	15.8	3504	6 US-10-428-961-39	Sequence 39, Appl1
45	262.4	15.6	3459	7 US-10-614-524-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-10-781-979-6
; Sequence 6, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziele, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AKMT-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1686)
US-10-781-979-6
Query Match 100.0%; Score 1686; DB 8; Length 1686;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAGTCCATGTTTACAGTAGTACGAAATTAAGTTAAATGAAGACAGATTAT 60
1 GTGAGTCCATGTTTACAGTAGTACGAAATTAAGTTAAATGAAGACAGATTAT 60
Db 1 GTGAGTCCATGTTTACAGTAGTACGAAATTAAGTTAAATGAAGACAGATTAT 60
QY 61 GAATATGATCAAGCGCCATTCTATAGATGTATGTATGATGAAATTAATCTCAGAA 120
61 GAATATGATCAAGCGCCATTCTATAGATGTATGTATGATGAAATTAATCTCAGAA 120
Db 61 GAATATGATCAAGCGCCATTCTATAGATGTATGTATGATGAAATTAATCTCAGAA 120
QY 121 AAAATTAATGTTATGGATGAATTAATTAATCTGCAAAACCACTTATGCTGTATCTA 180
121 AAAATTAATGTTATGGATGAATTAATTAATCTGCAAAACCACTTATGCTGTATCTA 180
Db 121 AAAATTAATGTTATGGATGAATTAATTAATCTGCAAAACCACTTATGCTGTATCTA 180
QY 181 CTCGAAATGAGACCTTTCTGGAATGATGAGATTCGATATGATATATATATATATAGGA 240
181 CTCGAAATGAGACCTTTCTGGAATGATGAGATTCGATATGATATATATATATATAGGA 240

Db 181 CTCCAAAATGAGACITTTCTGGGAATGATGGAATTCGGTAATGATATATATATGATAAGA 240
Qy 241 TCCAAATATCCATATTTTAAAGAAAAATTTCTACGATGCGGTGGAGCACGAGACATATAT 300
Db 241 TCCAAATATCCATATTTTAAAGAAAAATTTCTACGATGCGGTGGAGCACGAGACATATAT 300
Qy 301 GGAATCTATTTTCCAACTATATCTGTCAAAAAAATAGATAGTCTAAATTTAAACCATAT 360
Db 301 GGAATCTATTTTCCAACTATATCTGTCAAAAAAATAGATAGTCTAAATTTAAACCATAT 360
Qy 361 ACACGTTATCGAGTAAGAGGGTTGTGGAGTACTGTAAGATTTGAAATTTAATGTTAACA 420
Db 361 ACACGTTATCGAGTAAGAGGGTTGTGGAGTACTGTAAGATTTGAAATTTAATGTTAACA 420
Qy 421 CGTTACGGGAAAGAAATTTGATGCTATCATGMAATGTTCCAAATGATTTGGCCCTATATGAG 480
Db 421 CGTTACGGGAAAGAAATTTGATGCTATCATGMAATGTTCCAAATGATTTGGCCCTATATGAG 480
Qy 481 CCTAATCCCTTCATGTGAGATTTATCGCTGTGAATCATGCTCAGTATGTGAGCCAAAGG 540
Db 481 CCTAATCCCTTCATGTGAGATTTATCGCTGTGAATCATGCTCAGTATGTGAGCCAAAGG 540
Qy 541 TATCTTACACCAACAGATGATATGCTCCGATATGATGCAATGCGCCCAAAATATAGAT 600
Db 541 TATCTTACACCAACAGATGATATGCTCCGATATGATGCAATGCGCCCAAAATATAGAT 600
Qy 601 AGAAAGCATGTGAAGTGTACGATGCTCATTCATTTTCAATTTTGAACACCGGAGAA 660
Db 601 AGAAAGCATGTGAAGTGTACGATGCTCATTCATTTTGAACACCGGAGAA 660
Qy 661 GTAGATACAAATATACAAATGTAGTATTTGATTTTAAATTTCTAATCCAGATGGA 720
Db 661 GTAGATACAAATATACAAATGTAGTATTTGATTTTAAATTTCTAATCCAGATGGA 720
Qy 721 TACGCTACAGTAGGGAATCTAGAACTCATTTGAAGAGGACCACTAACAGGTGAACATG 780
Db 721 TACGCTACAGTAGGGAATCTAGAACTCATTTGAAGAGGACCACTAACAGGTGAACATG 780
Qy 781 GCACATGTGAACCAAAAGGAAAGAAATGGAACCAACATGAGAAATTTGTTGGGA 840
Db 781 GCACATGTGAACCAAAAGGAAAGAAATGGAACCAACATGAGAAATTTGTTGGGA 840
Qy 841 ACACAAACAGCCTATGATCCAGCAAAACAGGCTGTAGATGCTATTTTAAATGAACAA 900
Db 841 ACACAAACAGCCTATGATCCAGCAAAACAGGCTGTAGATGCTATTTTAAATGAACAA 900
Qy 901 GAGTTACATCATATTTACTTTAGATCATATTTCAAAACGCTGATGCACTGGTACAGTCG 960
Db 901 GAGTTACATCATATTTACTTTAGATCATATTTCAAAACGCTGATGCACTGGTACAGTCG 960
Qy 961 ATTCCCTATGTATACCAATTTGTTTACCGAATGCTCCAGATGCACTGATGATATAT 1020
Db 961 ATTCCCTATGTATACCAATTTGTTTACCGAATGCTCCAGATGCACTGATGATATAT 1020
Qy 1021 CAAGAGTTAAACGACGATCATGCAAGGTTAATATATATGATGCAAGAAATGTCTATA 1080
Db 1021 CAAGAGTTAAACGACGATCATGCAAGGTTAATATATATGATGCAAGAAATGTCTATA 1080
Qy 1081 ACAAATGTGACTTTTACCAAGAGTTACAGGATGGAACGCAACAGAAATGCCGCGGTA 1140
Db 1081 ACAAATGTGACTTTTACCAAGAGTTACAGGATGGAACGCAACAGAAATGCCGCGGTA 1140
Qy 1141 CAACAAATGATGAGCTTTCAGTATTAATTTCTATCAAAATTTGAGAGCGGGGTAATCTCA 1200
Db 1141 CAACAAATGATGAGCTTTCAGTATTAATTTCTATCAAAATTTGAGAGCGGGGTAATCTCA 1200
Qy 1201 AACTTGCAATGCTCAAGATCATCATGATGATGTTAGCTGTGATTTGCCAAAAAGAAAGA 1260
Db 1201 AACTTGCAATGCTCAAGATCATCATGATGATGTTAGCTGTGATTTGCCAAAAAGAAAGA 1260
Qy 1261 CCTGGAAGAGGATATGTAACGATGATGATTTGTAATGGAAGAGGAAACACTTAAAGTTC 1320
Db 1261 CCTGGAAGAGGATATGTAACGATGATGATTTGTAATGGAAGAGGAAACACTTAAAGTTC 1320

Qy 1321 ACTTCTTGGCAAGAGATATATGACAAAAACAGTAGAGGATTTCCGAGAAAGTATCGT 1380
Db 1321 ACTTCTTGGCAAGAGATATATGACAAAAACAGTAGAGGATTTCCGAGAAAGTATCGT 1380
Qy 1381 GTACGAGATTGAATATGAGAAACCGAAGTACATTTTATATATAGATGACATGAGTCTT 1440
Db 1381 GTACGAGATTGAATATGAGAAACCGAAGTACATTTTATATATAGATGACATGAGTCTT 1440
Qy 1441 TGTATGCAAGATATGATTAACATATATACCTGACACCGGGTATATGATATGACAAAGT 1500
Db 1441 TGTATGCAAGATATGATTAACATATATACCTGACACCGGGTATATGATATGACAAAGT 1500
Qy 1501 TATATGGAATTTATATCAAAATACTAGGATGTGATTTACCAAGGGTATACAAACAC 1560
Db 1501 TATATGGAATTTATATCAAAATACTAGGATGTGATTTACCAAGGGTATACAAACAC 1560
Qy 1561 TATACCAAGACTAGTATATGATATATCAAAATTTATCTAACAAATGATGACCTGCAT 1620
Db 1561 TATACCAAGACTAGTATATGATATATGATATCAAAATTTATCTAACAAATGATGACCTGCAT 1620
Qy 1621 TCCGTTGCAATGTAACCAAGGCAATACCTTGGCTGTACATGTAATCAAGATATTAAC 1680
Db 1621 TCCGTTGCAATGTAACCAAGGCAATACCTTGGCTGTACATGTAATCAAGATATTAAC 1680
Qy 1681 CGTTAA 1686
Db 1681 CGTTAA 1686

RESULT 2
US-10-781-979-1
; Sequence 1, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXM1-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5980
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-781-979-1

Query Match 100.0%; Score 1686; DB 8; Length 5980;
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 1686; Conservative 0; Mismatches 0

Qy 1 GTGAGTCTTATGTTTACAGTAGTACGAAAAATACGTTAAATATAGAAACGACAGATAT 60
Db 2309 GTGAGTCTTATGTTTACAGTAGTACGAAAAATACGTTAAATATAGAAACGACAGATAT 2368
Qy 61 GAAATGATCAAGCGCCATTTCTATATGATGATGTGACATGAAACAAATCTCAGAGAA 120
Db 2369 GAAATGATCAAGCGCCATTTCTATATGATGATGTGACATGAAACAAATCTCAGAGAA 2428
Qy 121 AAAATATGTTATGCGGATGGAATTAACCTGCAAAACAACTTGTGCTCGTATCTA 180
Db 2429 AAAATATGTTATGCGGATGGAATTAACCTGCAAAACAACTTGTGCTCGTATCTA 2488
Qy 181 CTCCAAAATGAGACITTTCTGGGAATGATGGAATTCGGTAATGATATATATCATAGA 240

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Db 2489 CTCCAAAATGAGACTTTTCGTGGAAATGATGGACATTCGGTAATGATATATCATAGGA 2548
QY 241 TCCAAATAATCTTAATTTTAAAGAAAATTTCTACAGATGCGTGAGACAGACATATAT 300
Db 2549 TCCAAATAATCTTAATTTTAAAGAAAATTTCTACAGATGCGTGAGACAGACATATAT 2608
QY 301 GGAATCTTAATTTTCCAACTTATCTGTCAAAAAATGATGACTTAAATTAATCAATAT 360
Db 2609 GGAATCTTAATTTTCCAACTTATCTGTCAAAAAATGATGACTTAAATTAATCAATAT 2668
QY 361 ACACGTTATCGAGTAAAGAGGTTGTGGAGATGATGAAGATTTGAAATTAATGATGA 420
Db 2669 ACACGTTATCGAGTAAAGAGGTTGTGGAGATGATGAAGATTTGAAATTAATGATGA 2728
QY 421 CGTTACGGGAAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTGGCTATATGCA 480
Db 2729 CGTTACGGGAAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTGGCTATATGCA 2788
QY 481 CCTAATCTCTTCAATGTGGAGATTTTGTGCTGTGAATCATGCTCATGATGTGAGCCAAAGG 540
Db 2789 CCTAATCTCTTCAATGTGGAGATTTTGTGCTGTGAATCATGCTCATGATGTGAGCCAAAGG 2848
QY 541 TATCTTACACCAACAGATGATGCTCCGATATGATGATGATGATGATGATGATGATGAT 600
Db 2849 TATCTTACACCAACAGATGATGCTCCGATATGATGATGATGATGATGATGATGATGAT 2908
QY 601 AGAAAGCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 2909 AGAAAGCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2968
QY 661 GTAGATCAAAATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 2969 GTAGATCAAAATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3028
QY 721 TACGCTACAGTGGGAAATCTAGAAGTCAATGAAGAGCACTAACAGATGATGATGATGAT 780
Db 3029 TACGCTACAGTGGGAAATCTAGAAGTCAATGAAGAGCACTAACAGATGATGATGATGATGAT 3088
QY 781 GCACATGTGAAACAAAAGGAAAGAAATGAAACACACATGAGAGAAACGTTGGAA 840
Db 3089 GCACATGTGAAACAAAAGGAAAGAAATGAAACACACATGAGAGAAACGTTGGAA 3148
QY 841 ACAACAACAGCTTATGATCAAGCAAAACAGGCTGTGATGATGATGATGATGATGATGAT 900
Db 3149 ACAACAACAGCTTATGATCAAGCAAAACAGGCTGTGATGATGATGATGATGATGATGAT 3208
QY 901 GAGTTAATCATATATCTTATGATCATATTAACAAAGCTGATGATGATGATGATGATGAT 960
Db 3209 GAGTTAATCATATATCTTATGATCATATTAACAAAGCTGATGATGATGATGATGATGATGAT 3268
QY 961 ATTCCCTATGATATCCATAATTTGTTACCGAATGCTCCAGATGATGATGATGATGAT 1020
Db 3269 ATTCCCTATGATATCCATAATTTGTTACCGAATGCTCCAGATGATGATGATGATGATGAT 3328
QY 1021 CAAGATTAAGCGCAGTATCATGCAAGTTATTAATTTATGATGATGATGATGATGATGAT 1080
Db 3329 CAAGATTAAGCGCAGTATCATGCAAGTTATTAATTTATGATGATGATGATGATGATGAT 3388
QY 1081 ACAATGTGATCTTACACAAGGATTAACAGGATGATGATGATGATGATGATGATGATGAT 1140
Db 3389 ACAATGTGATCTTACACAAGGATTAACAGGATGATGATGATGATGATGATGATGATGAT 3448
QY 1141 CAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db 3449 CAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3508
QY 1201 AACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 3509 AACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3568
QY 1261 CCGGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 3569 CCGGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3628
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QY 1321 ACTTCTTCCGAAGAGATATATGACAAAACAGTACAGTATTCGCCAGAAAGTATGCT 1380
Db 3629 ACTTCTTCCGAAGAGATATATGACAAAACAGTACAGTATTCGCCAGAAAGTATGCT 3688
QY 1381 GTACGATTTGAATGTAGAGAAACCGAAGGTACATTTTATATGATGATGATGATGATGAT 1440
Db 3689 GTACGATTTGAATGTAGAGAAACCGAAGGTACATTTTATATGATGATGATGATGATGAT 3748
QY 1441 TGTATGCAAGATATGATATCAATATATACCTGACACAGGTAATATGATGATGATGAT 1500
Db 3749 TGTATGCAAGATATGATATCAATATATACCTGACACAGGTAATATGATGATGATGAT 3808
QY 1501 TATATGCAATATATATCAAAATCTGACATGATGATGATGATGATGATGATGATGAT 1560
Db 3809 TATATGCAATATATATCAAAATCTGACATGATGATGATGATGATGATGATGATGAT 3868
QY 1561 TATAACCAAGACTAGTATATGATATATATCAATCAATCAATCAATCAATCAATCAAT 1620
Db 3869 TATAACCAAGACTAGTATATGATATATATCAATCAATCAATCAATCAATCAATCAAT 3928
QY 1621 TCCGTTGACATGTATACCAAGGATATCTGCTGTATCATGATGATGATGATGATGAT 1680
Db 3929 TCCGTTGACATGTATACCAAGGATATCTGCTGTATCATGATGATGATGATGATGAT 3988
QY 1681 CGTTAA 1686
Db 3989 CGTTAA 3994
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RESULT 3
US-10-929-754-4
; Sequence 4, Application US/10929754
; Publication No. US20050124803A1
; GENERAL INFORMATION:
; APPLICANT: ABDULLAH, MODH AMIR
; TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
; FILE REFERENCE: 22727/04179
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: 60/498,826
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patencin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-929-754-4

Query Match 54.3%; Score 914.8; DB 9; Length 4391;
Best Local Similarity 76.0%; Pred. No. 66-197;
Matches 1187; Conservative 0; Mismatches 357; Indels 18; Gaps 4;

QY 1 GTGAGTCTATGTTTAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Db 2799 GTGAGTCTATGTTTAAAGTACGATGATGATGATGATGATGATGATGATGATGATGAT 2858
QY 61 GAAATGATCAAGCGGCAATTTCTATGAAATGATGATGATGATGATGATGATGATGATGAT 120
Db 2859 GAAATGATCAAGCGGCAATTTCTATGAAATGATGATGATGATGATGATGATGATGATGAT 2918
QY 121 AAAATGATGTTATGAGATGAAATTAACATGCAAAACCACTTATGATGATGATGATGAT 180
Db 2919 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2978
QY 181 CTCGAAATGAGACTT-----TTCTGGGAATGATGATGATGATGATGATGATGATGAT 234
Db 2979 CTCGAAATGAGACTT-----TTCTGGGAATGATGATGATGATGATGATGATGATGAT 3038
QY 235 ATAGATCCATATATCTTATTTTAAAGAAATTTCTACAGATGCTGAGACACAGAGAC 294
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3039 ATTGAGCAGATTAATGCAACTTTTAAAGGAACTATCTGCAATGCTCGGGCGAGAGC 3098
QY 295 ATATATGGAATCTTATTTCCAACTATATCTGTCAAAAAATGATGAGTCTTAATTAATA 354
Db 3099 ATATATGGAACGATATTCCTCAACGTAATATATACAAAAAATGAGAAATCCAAATTAATA 3158
QY 355 CCATATACAGCTTATCGAGTAAAGAGGTTTGAGGAGATGATTAAGATTTGAAATTAATG 414
Db 3159 CCGATTTCGCGTTATCTAGTCAAGGAGATTTTGAGGAGATGATTAAGATTTGAAATTAATG 3218
QY 415 GTAACACGTTACGGGAAAGAAATTTGATCTATCATGAAATGTTCCAAATGATTTGGCTAT 474
Db 3219 GTAATGCGTTATGAAAAAGAAATTTGATACAGTAATGATGACCAATGACATACCGTAC 3278
QY 475 ATGACGCTTAATCTTCATGCT---GAGATTATCGCTGTGAATCATCGTCTCAGTATGTG 531
Db 3279 GTACCTTTATGCTCGGTCTGTACCAAAATTAATGATGTACCAACCGTATCCAAATAGG 3338
QY 532 AGCCAAAGGTTATCCACACCAACAGATGGAT-----ATGCTCCGATATGATGATGATGC 585
Db 3339 CATGTAGATATTTATATCAATGCAAGTTTCTCAGCTTTCTTACACATCCGATCTTGT 3398
QY 586 CCGCAAAATATATAGATAGAAAGCATGTGAAGTGTACGATCGTCAATCTTGAATTTTCAT 645
Db 3399 CAGGTACGCGCCGCAAAAAACATGTGTATGTCAATGATTTCTCATCAATTCAAATTTTCAT 3458
QY 646 ATTGACACCGGAAAGTATGATCAAAATGATGATGATGATGATGATGATGATGATGATGAT 705
Db 3459 ATTGATACGGGGGAGTATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 3518
QY 706 TCTATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
Db 3519 TCTTACCCGATGCTTACGCGACATTTAGTAATTTAGTAATTTAGTAATTTAGTAATTTAGTA 3578
QY 766 ACAGGTGAAGCATTTGCAATGTGAACAAAAAGAAAGAAATGGAACCAACATGAG 825
Db 3579 AGAGCGGAAGCATGTACATGTATAAACAAGAAAGAAATGGAATCAGCAATGAG 3638
QY 826 AAAAAAGCTTGGGAAACACACACACCTTATGATCCAGCAAAAGAGGCTGTAGATTCATTA 885
Db 3639 AAAAAAGCTTGGGAAACACACACACCTTATGATCCAGCAAAAGAGGCTGTAGATTCATTA 3698
QY 886 TTTTACAAATGAAACAAGATTTACATATCATATATCTTATAGATCAATTCAAATCCGCTAT 945
Db 3699 TTTTACAAATGAAACAAGATTTACATATCATATATCTTATAGATCAATTCAAATCCGCTAT 3755
QY 946 CGAGTGTACAGTGTATTCCTATGATATCAATTAATGTTATCCGATGCTCCAGATG 1005
Db 3756 GATTGGTACAGTGTATTCCTATGATATCAATTAATGTTATCCGATGCTCCAGATG 3815
QY 1006 AACTATGATGATATCAAGAGTTAAACGACGATATCATGCAAGGTTATTAATTAATGAT 1065
Db 3816 AACTATGATGATATCAAGAGTTAAACGACGATATCATGCAAGGTTATTAATTAATGAT 3875
QY 1066 GCACGAATGTATCAAAATGTGTGATCTTACACAAGATTTACAGGATGAGGATGAGGATGAG 1125
Db 3876 GCACGAATGTATCAAAATGTGTGATCTTACACAAGATTTACAGGATGAGGATGAGGATGAG 3935
QY 1126 GAAAATGCGCGGATCAACAAATGATGAGGCTTCAATTAATGATGATGATGATGATGATGAT 1185
Db 3936 GAAAATGCGCGGATCAACAAATGATGAGGCTTCAATTAATGATGATGATGATGATGATGAT 3995
QY 1186 GCGGGGATATCTCAAAATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1245
Db 3996 TCTGTAGATATCTCAAAATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 4055
QY 1246 GCAAAAAAGAGAGCTGAAAAAGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1305
Db 4056 GCGAAAAAGAGAGCTTGGAAAAAGGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 4115
QY 1306 GAAACACTTAAGTCACTTCTTGTGCAAGAGATATGACAAAAACAGTATGAGGATATTC 1365
Db 4116 GAAACACTTAAGTCACTTCTTGTGCAAGAGATATGACAAAAACAGTATGAGGATATTC 4175

QY 1366 CCAGAAAGTATGCTGTATGAGGATTTGAATATGAGAGAAACCGAAGGTACATTTATATAGAT 1425
Db 4176 CCAGAAAGTATGCTGTATGAGGATTTGAATATGAGAGAAACCGAAGGTACATTTATATAGAT 4235
QY 1426 AGCATCGATGCTTGTATGATCAAGATATGATATCAATATATATCACTGACACCGGATAT 1485
Db 4236 AGCATCGATGCTTGTATGATCAAGATATGATATCAATATATATCACTGACACCGGATAT 4295
QY 1486 ATGATATGACAAAGTTATATGCAAAATTTATATCAAAATTTATGAGGATGATATACCA 1545
Db 4296 ATGATATGACAAAGTTATATGCAAAATTTATATCAAAATTTATGAGGATGATATACCA 4355
QY 1546 GG 1547
Db 4356 GG 4357

RESULT 4
US-10-929-754-2
; Sequence 2, Application US/10929754
; Publication No. US20050124803A1
; GENERAL INFORMATION:
; APPLICANT: ABDULAH, MODH AMIR
; TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
; FILE REFERENCE: 22727/04179
; CURRENT APPLICATION NUMBER: US/10/929, 754
; PRIOR FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: 60/498, 826
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-929-754-2

Query Match 46.5%; Score 783.2; DB 9; Length 3684;
Best Local Similarity 72.2%; Pred. No. 4.2e-167;
Matches 1070; Conservative 0; Mismatches 388; Indels 24; Gaps 3;

QY 1 GTGAGTCCATATGTTTACAGTATGACGAAAAATACGTTAAATAATGAAACGACAGATTAAT 60
Db 2113 GTGAGTCCATATGTTTACAGTATGACGAAAAATACGTTAAATAATGAAACGACAGATTAAT 2172
QY 61 GAAATGATCAAGCGGCAATTTCTATAGAAATGATGTCAATGAAACAAATCCTCAGGAA 120
Db 2173 GAAATGATCAAGCGGCAATTTCTATAGAAATGATGTCAATGAAACAAATCCTCAGGAA 2232
QY 121 AAAATTAATGTTATGAGTGAATTAACCTGGCAAAACAACTTATGCTCTGTAATCTA 180
Db 2233 AAAATTAATGTTATGAGTGAATTAACCTGGCAAAACAACTTATGCTCTGTAATCTA 2292
QY 181 CTCGAAATGAGGACTT-----TCTGGGAAATGATGCAATTCGGTAATGATATATTC 234
Db 2293 CTCGAAATGAGGACTT-----TCTGGGAAATGATGCAATTCGGTAATGATATATTC 2352
QY 235 ATAGATTCATTAATCTTATTTTAAAGAAATTTCTACAGATCGCTGAGCAGAGAC 294
Db 2353 ATAGATTCATTAATCTTATTTTAAAGAAATTTCTACAGATCGCTGAGCAGAGAC 2942
QY 295 ATATATGGAATCTTATTTCCAACTATATCTGTCAAAAAATAGTATGATGATGATGATGATGAT 354
Db 2413 ATATATGGAATCTTATTTCCAACTATATCTGTCAAAAAATAGTATGATGATGATGATGATGAT 2472
QY 355 CCATATACGCTTATCGATATGAGGATTTGTGGAGATGATTAAGATTTGAATTAATG 414
Db 2473 CCATATACGCTTATCGATATGAGGATTTGTGGAGATGATTAAGATTTGAATTAATG 2532
QY 415 GTAACAGTTACGGGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474

Db 2533 GTTTCACGCTATGGGAAAGAAATGATGCCATCATGAAATGTTCCAGCTGATTTAAACTAT 2592
 QY 475 ATGCAGCCTAATCCTTCATGTGGAATATTCCTGTGAATCATCGTCTGATGTGAC 534
 Db 2593 CTGTATCCTTCTAC-----CTTTGATGTGAAAGGCTCTAATCGTTGTGAGACG 2640
 QY 535 CAAGGATCTCTACACCAACAGATGATATGCTCCCGAATATGTATGCAATCCCGCAAAAT 594
 Db 2641 TCCCGTGTGCGCGCTAACATTGGGAACACTTCTGATATGTTGATTCAGCCAAATATGAT 2700
 QY 595 ATAGATAGAAACATGTGAAAGTGTCCAGTCCATCCATTTGATTTTATATGACACC 654
 Db 2701 ACGGGAAGAAACATGTGTATGTGAGATTCCTCATATTTAGTTTCTCTATGATACA 2760
 QY 655 GGAGAAGTAGATACAAATACAAATAGGTATGATGTCTTATTTAAAAATTTCTAATCCA 714
 Db 2761 GGGGCAATTAGATACAAATAGAAATATAGGGGTTGGGTCATGTTTAAAAATCTTCTCCA 2820
 QY 715 GATGATACGCTACAGTACGAGGAATCTAGAAATCATTTGAAAGAGACCACTAACAGTGA 774
 Db 2821 GATGATACGCAATCATTAATATTAATTTAGAAATTTAGAAAGGCGCAATAGATGGGAA 2880
 QY 775 GGATGGCAATGTGAAACAAAAGAAAGAAATGGAAACAACATGGAGAAAAACGT 834
 Db 2881 GCACTGTCCGCGCTGAACACATGGAAAGAAATGGAAAGATCAATGGAGCAAAACGT 2940
 QY 835 TGGGAAACAAACAAGCCTATGATCCAGCAAAAACAGCTGTAGATGATATTTTCAAAAT 894
 Db 2941 TCGGAACACAAACAAGCATATGATGTAGGAAACAAGCAATGATGATCTTTATTCACAAAT 3000
 QY 895 GAACAAGA-----GTTACATATCATATTAATTGATCATATTTAAAAACGTATGCA 948
 Db 3001 GTACAGAGTAGAGCTTTTACAGTTTATGACACCTGCTCAATTCAGATCGTGTGATAT 3060
 QY 949 CTGGTACAGTCAATCCCTATGATATACAAATTTGGTTACCGAATGCTCCAGGTATGAAC 1008
 Db 3061 TTGGTACATCAATTCATATGTGTATGTATGATGATGATGATGATGATGATGATGATGAT 3120
 QY 1009 TATGATGATATCAAGAGTTAAACGCACTATCATGCAAGGTTATTAATTTATATGATGA 1068
 Db 3121 TATGATATCTATGTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
 QY 1069 CGAATGTATTAACAAATGTGATCTTACCAAGATTTACAGGATGATGATGATGATGATGAT 1128
 Db 3181 AAAAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3240
 QY 1129 AATGCCGGGTTCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
 Db 3241 AATGCAGACGTACAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
 QY 1189 GGGGATCTCAAAAACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1248
 Db 3301 GGGGATCTCAAAAACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3360
 QY 1249 AAAAAAGAGAGCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1308
 Db 3361 AAAAAAGAGAGAGCTGGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
 QY 1309 ACACCTTAAGTCACTCTTGCGAAGAGATATATGACAAAAACATAGAGGATTCCTCA 1368
 Db 3421 AATATGACGTTTACGTTTGTGTGAGAGAGATATATATGACAAACATAGAGGATTCCTCA 1380
 QY 1369 GAAAGTATCTGTATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
 Db 3481 GATACAGATCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
 QY 1429 ATCGAGTGTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
 Db 3541 ATTGAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3582

RESULT 5
 US-10-120-544A-3

; Sequence 3, Application US/10120544A
 ; Publication No. US20020182693A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANAKA, Masao
 ; APPLICANT: YOKOYAMA, Tomoko
 ; APPLICANT: AOYAI, Moriochi
 ; APPLICANT: HASEGAWA, Makoto
 ; APPLICANT: EHARA, Gaku
 ; APPLICANT: KIMURA, Masaharu
 ; APPLICANT: NISHIHASHI, Hideji
 ; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
 ; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
 ; FILE REFERENCE: OP135
 ; CURRENT APPLICATION NUMBER: US/10/120,544A
 ; PRIOR FILING DATE: 2002-04-12
 ; PRIOR APPLICATION NUMBER: JP 2001-115754
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: JP 2001-203463
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 4359
 ; TYPE: DNA
 ; ORGANISM: Bacillus popilliae
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (282)..(4229)
 US-10-120-544A-3
 Query Match 22.8%; Score 384.2; DB 5; Length 4359;
 Best Local Similarity 58.0%; Pred. No. 1.8e-76;
 Matches 805; Conservative 0; Mismatches 528; Indels 54; Gaps 5;
 QY 1 GTGAGTCCATGTTTACAAAGTAGTACGAAAAATAGCTTAAAAATAGAAACGACAGATTAT 60
 Db 2337 GTGAACCATTTGTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2396
 QY 61 GAATATGATCAACGCGCCATTTCTATAGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Db 2397 GAGATGATCAACGCGCCACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2453
 QY 121 AAAATATGTTATGAGATGAATAAACTGGCAAAACAATTAGTCACTCTGTATCTTA 180
 Db 2454 AAAATATGTTATGAGATGAATAAACTGGCAAAACAATTAGTCACTCTGTATCTTA 2513
 QY 181 CTCCAAAATGAGACTTTCT-----GGGAATGATTGAGACA 216
 Db 2514 CTGCTCAATGGGAATTTTGCATGATCTATATATCCAGCTCTGAGAGAGGAGAAATCCATGGAAA 2573
 QY 217 TTCGTAATGATATATATCATATGATCAATATATCTAATTTTAAAGAAATTTCTACAG 276
 Db 2574 ACAAGTCGCAATGTTATCATCCGTCAAGATTAACCGATTTTAAAGCGCATTTATCTCAGT 2633
 QY 277 ATGCTGAGACGAGACATATATGAAAC-----TCTATTTCCAACTTATCTGTCAA 330
 Db 2634 ATGGCGGGTGCAGAAAGATATGAGGCCAACATGATACCTTCCCAAGTATCTATCA 2693
 QY 331 AAAATATGATGATCAATTAATTAACCATATACGTTATCGAGTAAAGAGGTTTGGGA 390
 Db 2694 AAAATATGAGAGCCAAATTTAAAGCATATATACAGGTATTAAGTGGCGGGTTGTGGT 2753
 QY 391 AGTATTAAGATTTGAAATTAATGTTAAACAGTTACGGAAGAAATGATGATGATGATGATGAT 450
 Db 2754 ACGAGAAAGCTCTAGAGTGTGTGTTACAGCTATTAATGAAGAGATGATGATGATGATGAT 2813
 QY 451 AATGTTCAATGATTTGGCTTATATGACAGCTTAATCTTCAATGTGAGAGATTTAGCTGT 510
 Db 2814 GATGTACCGAGATTAATATCCGATCGCGCATCTCTGTCTGTGCGAATTTGATGATGATG 2873
 QY 511 GATCATGCTC-----TCAGTATGTGAGCGAAGGATCTTACACCAACA 555

Db 2874 AAGCCATATGCTATCACTTTACTCCAGATGTAACCTGAGTTTAAATCAGATG 2933
Qy 556 GATGATATGCTCCCGATATGATGATGCGCCAAATATGATGAAAGATGTGAAG 615
Db 2934 CAACCATCTCTTGGCCACCAATCAGATGATGATGATGATGATGATGATGATG 2993
Qy 616 TGTCAAGATGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATG 675
Db 2994 TGTCAAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 3053
Qy 676 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 735
Db 3054 GATTTGGCATTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 3113
Qy 736 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 795
Db 3114 GATTTGGCATTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 3173
Qy 796 AAGGAAAGAAATGGAACCAACATGGAAGAAAGAAAGAAAGAAAGAAAGAAAG 855
Db 3174 AGAGAAAGAAATGGAACCAACATGGAAGAAAGAAAGAAAGAAAGAAAGAAAG 3233
Qy 856 GATCCAGCAAAACAGCTGTAGATGATGATGATGATGATGATGATGATGATGATG 909
Db 3234 GATGCGCCAAACAGCTGTAGATGATGATGATGATGATGATGATGATGATGATG 3293
Qy 910 TATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 969
Db 3294 TTTGAAACCAACATGATGATGATGATGATGATGATGATGATGATGATGATG 3353
Qy 970 GTATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1029
Db 3354 GTATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3413
Qy 1030 AACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1089
Db 3414 AACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3473
Qy 1090 GACTTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1149
Db 3474 GCGTTTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3533
Qy 1150 GATGAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1209
Db 3534 TATGGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3593
Qy 1210 GCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1269
Db 3594 ATCGAAGCAATGCGGATGATGATGATGATGATGATGATGATGATGATGATG 3653
Qy 1270 GGGTATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1329
Db 3654 GGGTATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3713

RESULT 6
US-11-091-654-3
; Sequence 3, Application US/11091654
; Publication No. US20050172355A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: Insecticidal effect on scarabaeidae insects and

; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: 09135
; CURRENT APPLICATION NUMBER: US/11/091,654
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-11-091-654-3

Query Match 22.8%; Score 384.2; DB 10; Length 4359;
Best Local Similarity 58.0%; Pred. No. 1.8e-76; Indels 54; Gaps 5;
Matches 805; Conservative 0; Mismatches 528;

Qy 1 GTGAGTCTATGTTTACAGATGATGATGATGATGATGATGATGATGATGATGATG 60
Db 2337 GTGAGTCTATGTTTACAGATGATGATGATGATGATGATGATGATGATGATGATG 2396
Qy 61 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Db 2397 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2453
Qy 121 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
Db 2454 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2513
Qy 181 CTCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 216
Db 2514 CTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2573
Qy 217 TTCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 276
Db 2574 ACAAGTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2633
Qy 277 ATGCGTGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 330
Db 2634 ATGCGTGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2693
Qy 331 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 390
Db 2694 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2753
Qy 391 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 450
Db 2754 AGCAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2813
Qy 451 AATGTCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 510
Db 2814 GATGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2873
Qy 511 GAATCATGTC-----TCAGATGATGATGATGATGATGATGATGATGATGATGATG 555
Db 2874 AAGCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2933
Qy 556 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 615
Db 2934 CAACCATCTCTTGGCCACCAATCAGATGATGATGATGATGATGATGATGATGATG 2993
Qy 616 TGTCAAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 675
Db 2994 TGTCAAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3053
Qy 676 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 735

Db 3054 GATTGGGCGATTGGGTGATCTTCAAAATCTGTGCCACAGATGTTACCGCAAGCTTAAGT 3113
Qy 726 AATCTAGAAAGTCATTGGAAGAGACCACTAACAGGTGAAGCATGGCAGATGTGAACA 795
Db 3114 GATTGGAAAGTATTGGAAGAGAGAGCGCTGGGTGTGGAAGCATTTGAACTTGTCAAGAA 3173
Qy 796 AAGGAAAAAATGGAACACACATGAGGAAAAAAGCTTGGGAAACAAACAGCTT 855
Db 3174 AAGGAAAAAATGGAAGATGAGAGAGAGAGACCTGTTCCAAACGAAACAAATAT 3233
Qy 856 GATCCAGCAAAACAGCGCTGTAGATGCAATTATTACAA-----TGACAAAGATTAC 909
Db 3234 GATGGGGCCAAACAGCGGTGTAGTGGGTATTTCACAAACAGCGCTATGAAAAATTGAAG 3293
Qy 910 TATCATATTACTTTAGATCATATTCAAAACGCTGATGACGTGTACATGATTCCTTAT 969
Db 3294 TTGCAAAACAACATCTCCAAATATTTGTATGCTGATCATCTGTGAGTCGATTCCTTAT 3353
Qy 970 GTATACATTAATTGGTTACCGAATGCTCAGGTATGAACTATGATGATATCAAGTTA 1029
Db 3354 GTATATTAATTAATGATGACCGAAGTTCCAGGTATGAACTTACGAATCTTATCAGAGCTA 3413
Qy 1030 AACGACGATCATGCAAGGTTATATATTATATGATGACGAATGTCAATTAACAAATGCT 1089
Db 3414 AACATCTCTGTCAGAAATCGCTTATCTATATGACGACGGAATCTGATTAATAATGGG 3473
Qy 1090 GACTTTACACAGATTACAGGATGACGCAAGCAAGAAATGCCGGTACACAAATG 1149
Db 3474 CGCTTTAGCAATGGGCTTATGATTTGAGGACAGCTACCCCGCATGACAGATGGAACAA 3533
Qy 1150 GATGAGCTTCAGTATTAAGTTCTATCAAAATTTGAGGCGGGGTATCTCAAACTTGCT 1209
Db 3534 TATGAAATCTGTACTCGTGTGCGCAATGTGGATGCCAATGTGTGCGAAGATCTTTGT 3593
Qy 1210 GCTCAAGATCATGATGATGATGTTAGTGTGATTTGCCAAAAAAGAGACCTGGA 1269
Db 3594 ATGCAACATGCGGTTATGATTTGCTGTCAAGGCAAGAAAGAAATCCGGAGCT 3653
Qy 1270 GGGTATGTAACGATGATGATTTGTAATGAAAGCAGAAACATTAAGTTCACTTCTGC 1329
Db 3654 GGCAATGTTACCTTCAGTACGTGTGCAACATGTGCAAGTGTGAGCTTTACTTCTGC 3713
Qy 1330 GAAGAG 1336
Db 3714 GATATAG 3720

RESULT 7
US-10-089-678-2
; Sequence 2, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis*
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(3501)
; OTHER INFORMATION:
US-10-089-678-2

Query Match 22.5%; Score 379; DB 5; Length 3504;
Beet Local Similarity 56.7%; Pred. No. 2.5e-75;
Matches 839; Conservative 0; Mismatches 555; Indels 87; Gaps 4;
Qy 22 AGTACGAAATATACCTTAAAAATAGAAACGACAGATTATGAATGATCAACGGCCATT 81
Db 2062 AGTAAAAAGATGCTTACAGACAGATGTAACGATTTATCAAGTATCAACGGCCAAAC 2121
Qy 82 TCTATGAATGATGTCAGATGAAACAAATCTCAGAAAAAATATATGATGATGAA 141
Db 2122 TTAGTGAATGCTTCCGATGATGATATACCAATGAAAAAGATGTTATGGATGCA 2181
Qy 142 ATAAAAAGGCAAAACACTTATGATGATCTGTATCTATCTACCAAAATGAGAACCTTTCT 201
Db 2182 GTGAAAGGGCGAAACGACTGTTGAGGACGTAATCTTCAAGATACAGGCTTTTAT 2241
Qy 202 GGAATGAT-----TGACATTCGGTATGATATATATCATAGATCCAAATAT 249
Db 2242 AGGATTTAATGCAAAACGATGACGGGAAGTACGGAAATGAGATTGCGGAAGAGAT 2301
Qy 250 CCTATTTTAAAGAAAAATTTCTACAGATGCGTGAGACAGACATATATGAACTCTA 309
Db 2302 GTTCTGTTAAAGATCGTTGCTGCTTGTGACAAATGCGAAGATGATGATACAGAAACA 2361
Qy 310 TTTCCAACTTATCTGTCAAAAAATAGATGATCTAAATTTAAACCATATACAGTTAT 369
Db 2362 TATCCAAAGTATCTTATCAACAAATAGATGATCACTTTTAAACCATATACAGATAT 2421
Qy 370 CGAGTAAAGGGTTGTGGAGATGTAAGATTTGAATTAATGATGTAACGTTACGGG 429
Db 2422 AAATTAAGGTTTATTAAGAAATGATCAAGATTTAGAGATTAATTAATTAATGATCGG 2481
Qy 430 AAAGAAATGATGATCATGATGATGTTCCAAATGATTTGGCCTATATAGCAAGCTTATCT 489
Db 2482 GCAATTCAAATGTCAAAAATGATACAGATATCTCTGCGAGATGATCTCCCTGTCAAT 2541
Qy 490 TCAATGAGATTAATGCGCTGTCAATCTGTCTCAATGATGATGATGATGATGATGATGAT 549
Db 2542 TCTGTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2582
Qy 550 CCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
Db 2583 -----AAGCGGAATTTAGCACTCGAAACAAATGATGATGATGATGATGATGATGAT 2622
Qy 610 GTGAAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
Db 2623 AATATGCTTTCATGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2682
Qy 670 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
Db 2683 AATGAAATATACAGAAATTTGGTGTGATTTAAATTTCCCAACAAATGATGATGATGATGAT 2742
Qy 730 GTAAGGAATCTGAAGTATGTAAGAGGACACTTACAGATGATGATGATGATGATGATGAT 789
Db 2743 CTAGGAATCTGGAATGTAAGAGGCGCATTTGTGAGGGAACATTTAGACAGACA 2802
Qy 790 AAAAGAAAGAAAGAAATGGAACACACATGAGGAAAAAAGCTTGGGAAACACAAACA 849
Db 2803 CAAACAAAGAAACAAATGGAAGGCAAAATGGAAGAAACGTTGGGCACTCAGAAAAA 2862
Qy 850 GCTATGATCAGCAAAACAGCGCTGTAGATGATGATGATGATGATGATGATGATGATGAT 909
Db 2863 GCATTTATGACAGCAAGCAACCATGATGCTTTTATTTGCGAGATTTATCAAGCCAAAAA 2922
Qy 910 TATCATATTACTTTGA-----TCATATCAAAACGCTGATGATGATGATGATGATGAT 963
Db 2923 CTTAATTTCTGTGTGAATGTCAGATATGTTGGACGCCAAACCTTGTACAGTCAAT 2982
Qy 964 CCTATGATACCAATATTTGTTACCGAATGCTCCAGATGATGATGATGATGATGATGATGAT 1023
Db 2983 CCTAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3042

Accession	Sequence	Position
Dd	GGAGACGGATATGTGATCATCCGTGATGTGGCAATCAGACAGAAACCTCACATTTAAT	3528
Qy	1324 TCTTGGCAAGAG-----GATATATGACAAAAACA	1353
Dd	3529 ATATGTGATGATGATACAGGTGTTTATCTGTCTATCAAACTAGCTATATCAGAAAAACA	3588
Qy	1354 GTAGAGGATATTTCCAGAAAGTGATCGTGTCGGAATTGAAATAGAGAAACCGAAGGTACA	1413
Dd	3589 GTGGATTCACCTCATCTACAGAGCAAGATTGGATTGACATGAGTGAGACCGAAGGTGTA	3648
Qy	1414 TTTTATATAGATGATCGATGGTGGCTTGTATGCAAGATA	1454
Dd	3649 TTCAACATAGAAAGTGATGAACCTCGTGTAGAAAGAGGTA	3689

RESULT 9
US-09-756-526A-3

; Sequence 3, Application US/09756526A
; Patent No. US20020038005A1

GENERAL INFORMATION:

APPLICANT: Jana, Wojciechowska

APPLICANT: Evgeny, Lewitin

APPLICANT: Ludmila, Revina

APPLICANT: Igor, Zalunin

APPLICANT: GALINA, CHEBOKININA
TITLE OF INVENTION: NOVEL DELTA

FILE REFERENCE: S-30913A

CURRENT APPLICATION NUMBER: US/09/756,526A

! CURRENT FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: US 60/

PRIOR FILING DATE: 2000-01-07

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; NUMBER OF SEQ ID NOS: 5
SOFTWARE: BioEdit version 3

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; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 3

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LENGTH: 4896

TYPE: DNA

ORGANISM:

FEATURE:

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; NAME/KEY: SOURCE
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LOCATION

OTHER INFORMATION: Be

NAME/KEY: CDS

NAME/KEY: CDS
LOCATION: (1129) .. (4458)

OTHER INFORMATION: produc

; PUBLICATION INFORMATION:

AUTHORS: Wojciechowska, et al.

TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from *Bacillus*

TITLE: churinglensis bsp. flint

JOURNAL: FEBS Lett.
VOLUME: 453VOLUME: 433
ISSUE: 12

PAGES: 46-48

DATE: 199

; DATABASE

US-09-756-526A-3

100

Query	Match	18.6%
Post-1000	61.1%	5.4%

Best Local Store
Matches 809:

Query Match 18.6%; Score 313; DB 3; Length 4896;

Best Local Similarity 54.9%; Pred. No. 2.8e-60;

Matches 809; Conservative 0; Mismatches 595; Indels 69; Gaps 7;

Qy	CGAAAAATACCTTAAAAATAGAAACGACAGATTGTGAAATGATCCAGCGGCACATTTCTA	85
Db	CACACAAACGCTTTGAAAATGACGTAACTGATTACATGATCAATGGCAACTTAG	3061
Qy	26	
Db	3002	
Qy	86	145
Db	3062	3121
Qy	146	198
Db	3122	3181

QY	199	-----TCGGGAATGATTGGCATTCGCGTATGATATTATCATAGATCCAAATATCTTA	253
Db	3182	TAAACGCTGAAAAATAGTTGGACACCAATAACAGGTGTCACAATCATATGAAAGAACCCAT	3241
QY	254	TTTTTAAAGGAAAAATTCTACAGATGCGTGAGACGACGACATATATGGAATCTATTTTC	313
Db	3242	TGTTAAAGGCGGTGCTATTCAATTATCAGCCGCGAGGAGTAAAA-----CTTTC	3292
QY	314	CAACCTATCTGTCAAAAAATAGATGATGCTAAATTAAAACATATACAGTTATCGAG	373
Db	3293	CAACTTATCTGTACAAAAAATAGATGATCTTATTAAAACTTATACGTTATCAAC	3352
QY	374	TAAGAGGCTTGTGGGAAATGTAAGATTGAAATTATGCTTAAACAGCTTACGGGAAG	433
Db	3353	TAAAGAGATTGTGAAAGTAGTCAAGATTGAACTCGATTTGTGTACGCTACGGG---G	3409
QY	434	AAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGACGCTAACTCTTCAT	493
Db	3410	CACACGATTTGTATGATGATGATGCGCCGCGACTTG---AAATCTCAGTTTACTGTGCC	3466
QY	494	GTGAGATTTATCGCTGTGATCATCTGTCAGTATGTGAGCCAAAGGATCTTACACCA	553
Db	3467	CTATCAATCCCTGTGAGGAAATATAGAACGCGTTAGATCTATCTGTGTGCG-----	3520
QY	554	CAGATGATATGCTCCGATATGTATGATGATGCGCCGCAAAATATATGATGAAAGCATGTA	613
Db	3521	TTGATCGTTGTAAACAATCCAAATTATGTAAATTGAGTGCAGATGTAAAGGCGTATCAG	3580
QY	614	AGTGTACAGATCGTCATCCATTTGATTTTCAATTTGACACCGGAGAAATAGATCAATA	673
Db	3581	TGAATGAGATCCACGCAATTTTCATTCATTCATTTGATGATACAGTATCTACGATTAATATA	3640
QY	674	CAATGTAGTATGATGTCTTATTTAAAAATTTTCTAATCCAGATGATACCTACAGTAC	733
Db	3641	GAAATTTAGGATTTGGATTATTTTAAAAATTTGACACACGAGCGCTATGCCAATTTGCG	3700
QY	734	GGAATCTTGAAGTCAATGGAAGAGACCACTAACAGTGAAGCATTTGCACTGTGAAC	793
Db	3701	GTAATCTTGAATGTATGAAATTGGGACCATTATCTGAGGAAGCGTTAGCAAAATACAC	3760
QY	794	AAAAAGAAAAAATGGAACACACATGAGAAAAAAACGTTGGGAAACACACAAGCT	853
Db	3761	GGAAGAAACAAAAATGGGAAAAAAACAAACCAAAAAAGGAAGAAAGCTGCAAAATTTAT	3820
QY	854	ATGATCCAGCAAAAACGCGTGTAGATGATTAATTTACAAATGAACAAG-----AGTTAC	907
Db	3821	ATGCACTGTCAAGACAAACAATTAATCAATTAATTCGCCGATTCACACAGCTACAAATTTAA	3880
QY	908	ACTATCATATTAATCTTATGATCATATTCCAAAACGCTGATCGATCGTACATGCCATTCCT	967
Db	3881	GATTTGATACAGAAATTCCTCAATTTTTTATCGGACAGTAATAACTGTCTATAAATTTGAG	3940
QY	968	ATGTATACATTAATTGTTACCGAATGCTCAAGTATGAATATGATATATCAAGAT	1022
Db	3941	ATGTATATAGGAAGTTTATCTGTATCCAGAGTTAAATTAATGATTTATTTATGAAAC	4000
QY	1028	TAAACGACGCTATCATGACAGGTTATAATTATATGATGACAGAAATGCTCAATCAATG	1087
Db	4001	TTGAAATATGAAATTCAGATGCAATGTGATTTATATGACGCTCGCAATTCCTGACAAATG	4060
QY	1088	GTGACTTTTACCAAGATTACAGGATGCGACGCAACGAAATGCGCGGTACACACAA	1147
Db	4061	GGAGTTTAAAGAAATGGTTTGGCGAATTTGAGATGGCTTATCAAAATACGAATTAAGGCABA	4120
QY	1148	TGATGAGCTTCAGTATTAAGTTCTATCAAAATTTGAGAGCGGGGTATCTCAAACTTGC	1207
Db	4121	TCCAGGCGCAATCCGATGTGTACTCTAGGCTGAAATGCGCAGGTGCACAATCTCTTA	4180
QY	1208	ATGCTCAAGATCATCATGATATGTGTGTAGCTGTGATGTCGCAAAAAAGAAAGACCTGGAA	1267
Db	4181	ATGTGAAACCTGATCATAGGATATGATATTAACGTGTACACGCAAAAAAGAAAGAAATTTGATA	4240
QY	1268	AAGGGTATGTAACGATGATGATTTGTATGAGAAACAGAAACAATTAAAGTTCACTTCTT	1327

Db 4241 ATGGCTATGTGCAATCTTGACTGTGCAATCATATTGATGATGCTTGAATTAGTCTT 4300
Qy 1328 GCGA-----AGAGGATATATGACAAAACAGTNG 1357
Db 4301 GTGATTCAGGTTTCACTACTTCTTCTAATGAAATGACGCTATGTATCAAAAACGTTAG 4360
Qy 1358 AGGTATTCACGAAGATGATCGTACGATTGAAATAGAGAAACCGAAGGTACATTTT 1417
Db 4361 AATTTTCCCATATACCATTCAAATTCGATTTGAAATCGCGCAAAACCGAAGTACGTTT 4420
Qy 1418 ATATAGATGATCGATCGATGTTGTTGTATGCAAG 1450
Db 4421 ATGTAGAAAGTGTGACCTAATTCGAATGAGAG 4453

RESULT 10
US-10-345-020-3
; Sequence 3, Application US/10345020
; Publication No. US20030150018A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeny, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zalunin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913B
; CURRENT APPLICATION NUMBER: US/10/345,020
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/175,158
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4896
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(4896)
; OTHER INFORMATION: Bacillus thuringiensis subsp. finitimus strain VPM B-1161 (taxon
; OTHER INFORMATION: :29337
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1129)..(4458)
; OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
; PUBLICATION INFORMATION:
; AUTHORS: Wojciechowska, et al.
; TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
; TITLE: thuringiensis ssp. finitimus
; JOURNAL: FEBS Lett.
; VOLUME: 453
; ISSUE: 12
; PAGES: 46-48
; DATE: 1999-06-18
US-10-345-020-3

Query Match 18.6%; Score 313; DB 6; Length 4896;
Best Local Similarity 54.9%; Pred. No. 2.8e-60;
Matches 809; Conservative 0; Mismatches 595; Indels 69; Gaps 7;

Qy 26 CGAAAAATACGTTAAATATAGAAAGACAGATTATGAAATGATCAAGCGGCATTCTTA 85
Db 3002 CAACAAAGCGTTGAAATGACGTAACGATTATCACATTGATCAAGTGCAAACTTAG 3061
Qy 86 TAGATGTATGTACAGATGAACAAATCTCAGAGAAAAATATGTTATGGATGAATTA 145
Db 3062 TAGATGTATGTACAGATGAACAAATCTCAGAGAAAAATATGTTATGGATGAATTA 3121
Qy 146 AACTGGCAAAACCACTTATGTCAGTCTCGTATCTTACTCCAAAATGAGACTTT----- 198
Db 3122 AATTCGCAAAACCACTTATGTCAGTCTCGTATCTTACTCCAAAATGAGACTTTTAACAATC 3181

Qy 199 -----TCGGGAATGATTTGACATTCGGTAATGATTTATATCATATGATCCAAATATCCTA 253
Db 3182 TAAACGCTGAAATATGTTGGACAGCAAAATACAGGTCTCAATCATTTGAAGAGACCAT 3241
Qy 254 TTTTAAAGAAAATTTCTACAGATGCGTGAGACAGACATATATGAACTCTATTTTC 313
Db 3242 TGTATAAAGGCGGTCTTCAATTTATCAGCCGAGAGGATGAAAA-----CTTTC 3292
Qy 314 CAACCTATATCTGCAAAAATATAGATGCTAATTTAAACATATACAGTTATGAG 373
Db 3293 CAACCTATCTGTACAAAATATAGATGATCTTATTTAAACCTTATACAGTTATCAAC 3352
Qy 374 TAAAGGGTTTGGGAAAGTATGTAAGATTTGAAATTTAATGTAACATTTACGGGAAG 433
Db 3353 TAAAGGATTTGTAAAGATGATGATGATTTAGAACTCGATTTGTAGCTACGG---G 3409
Qy 434 AAATTTATGCTATCATGATGATGTTCCAAATGATTTGGCTATATGCAACCTAATCTTCAT 493
Db 3410 CAACAGACATTTGATATGATGATGCTCCGCGACCTTG---AAATCTCAGTTACTGTGCC 3466
Qy 494 GTGAGATTTATCGCTGTGAATCATCTCTCATGTATGAGCAAGGATTCCTACACAA 553
Db 3467 CTATCAATCTTGTGAGGAAATGAAACACGCTTAGATCTACTGTGTGCGC----- 3520
Qy 554 CAGATGATATGCTCCGATATGTATGATGATGCTCCGCAAAATATATGATGAAGCATGGA 613
Db 3521 TTGATCGTTTAAAGCAATCCAAATTTATGTAATTTACGTGCAAGATGTAAGGCTGATCAAG 3580
Qy 614 AGTGCAGATCGTATCATCTTATTTCAATTTGACACCGGAAAGTATGATCAAAATA 673
Db 3581 TGAATGAGATCCACAGCATTTTCATTCATTTGATGATGATGATGATGATGATGATGAT 3640
Qy 674 CAAATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 733
Db 3641 GAAATTTAGGATTTGATTTATTTTAAATTTGACACGACGAGCTATGCAATCTTTCG 3700
Qy 724 GGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793
Db 3701 GGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3760
Qy 794 AAAAGAAAAGAAATGGAACACACATGAGAAAAAAGTTGGGAAAACCAACACAGCTT 853
Db 3761 GGAAGAAAAGAAATGGAAGAAAACCAACCAAAAGGAAAGAGTCAAAATTTAT 3820
Qy 854 ATGATCCAGCAAAACAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
Db 3821 ATGATCCAGCAAAACAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3880
Qy 908 ACTATCATATTAATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967
Db 3881 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3940
Qy 968 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1027
Db 3941 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4000
Qy 1028 TAAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1087
Db 4001 TTAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4060
Qy 1088 GTGACTTTACCAAGGATTTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1147
Db 4061 GGGAGTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4120
Qy 1148 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1207
Db 4121 TCAAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4180
Qy 1208 ATGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1267
Db 4181 ATGGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4240

Query Match	18.2%	Score 306.4	DB 5	Length 4359
Best Local Similarity	55.4%	Pred. No. 8.3e-59		
Matches 817; Conservative		0; Mismatches 516		Indels 141; Gaps 6

Qy	1	GTGAGTCCCTATGTTTACAGTAGTACGAAAAATACGTTAAAAATAGAAACGACAGATTAT	60
Db	2203	GTGAACCACTTTGTTTACAGATGGATCGAAAAAGGGGCTAAAAGAAAGACACGACCGATTAT	2262
Qy	61	GAATATGATCAAGCGGCCATTTCTATAGATTATGTCAGATGAACAAATCTCAGGAA	120
Db	2263	GAGATTGATCAAGCCGCCAACGTGTAGATTGTATATCGGAG--AGTGTGACATGAG	2315
Qy	121	AAAAATAAATGTTATGGGATGAATAAATACGGCAAAACAACTAGTCAGTCTGTATATCA	180
Db	2320	AAAAATGATCTCTTATGATGAAATAAAAATATGCAAAACAACTACGCCAACGCCGCAATTTA	2377
Qy	181	CTCCAAAATGAGACTTTTCT-----GGGAATGATTGGACA	216
Db	2380	CTGCTCAATGGGAATTTGCATATCTATATCCAGCTCTGAGAGGGAGATCATGGAAA	2433
Qy	217	TTCCGTAATGATATATATCATAGGATCCAAATATCTATTTTAAAGAAAAATTTCTACAG	276
Db	2440	ACAACTCCGAATGTTACGATCCGTCAAGATAACCGGATTTTAAAGCCATTATCTCAGT	2495
Qy	277	ATGCGTGGAGCAGACATATATATGAAC-----TCTATTTCCAACCTATATCTGTCA	330
Db	2500	ATGGCGGGGTGCACGATATCGAGGCGACCAATGATATAGTTCCCAACGATATCTATCA	2555
Qy	331	AAAAATGATGAGCTCTAAATTAATAAACCATATACAGTTATCGAGTAAAGGGTTTGTGGGA	390
Db	2560	AAAAATGATGAGCCAAATTAAGCCATATACCGGTATTAAGTCCGGGGTTTGTGGC	2613
Qy	361	AGTAGTAAGATTTCAAAATTAATGTGAACAGTTACGGGAAGAATGATCTCTATCATG	450
Db	2620	AGCGCAAAAGATCTGAGCTGTGTGTTACCGCTTAATATGAAGAAAGTTGATCGAATTTTA	2677
Qy	451	AATGTTCCAAATGATTTGGCCTATATGACGCTTAATCCTTCATGTGAGATTAATGCTGT	510

Db	2680	GATGTACCGGATAATATATCCCGCATGCCCGCATCTCTGTCTGCGGTGAATTTGATCGATGC	2739
OY	511	GAATCATCGTC-----TCAGTATGTAGAGCCAMG-----	539
Db	2740	AAGCCCTATTGTATCCACCTTTACTTCAGAAATGTAACTCGTAGTTTATTAATCAGATG	2799
OY	540	-----	539
Db	2800	CAACCATCTCTTGCCACCAATCAGATGTGATTACATAAATATGAACACGACGACG	2859
OY	540	-----GTATCTCAACACCAACAGATGATGATGCTCCCGATATGATGATGCCG	588
Db	2860	AGTACTACCAATGAATCTCTAGCATGAATATCTCTCCCTTAAGCCTGAATAATGATCAAGC	2919
OY	589	CAAAATATAGATAGAAAGCATGTGAAGTGCACATCGTCATCCATTTGATTTTCATATT	648
Db	2920	AGTGGATTCCGACAGAAACATCGCAAAATGTATCAACGCGCATCAATTTGAGTTCCACATT	2979
OY	649	GACACCGGAGAAGTATGATCAAAATATCAAAATGTAGTATGATATGATCTTATTTAAATTTCT	708
Db	2980	GATACCCGGACAATTCGATTTGTGTGAAGATTTGGCATTTGGGTGATCTTCAAAATCTGT	3039
OY	709	AATCCAGATGGATACGCTCAAGTAGGAGATCTTAAGATCATTTGAAGAAGCACACTAACA	768
Db	3040	GCCACAGATGATATCGCAAGCTTGATGATGATTTGGAAATGATTAAGAAAGAGACCTGGG	3099
OY	769	GGTGAAGCATTTGSCACATGTGAAAACAAAGGAAAGAAATGGAACACACATGAGAGAA	828
Db	3100	GTCCGAGCCTTAGAACTTGTCAAGAAAAGAAAAGAAATGGAACATCATGAAAGAGACAG	3159
OY	829	AAAGCTTGGGAAACACAAACAGCCTTATGATCCACAAAACAGCGGTGATGATGATTTATT	888
Db	3160	CAGTGTTCGCAAGAAACACAAATATGATGCGCCAAACATGCGGTGATGCGCTATTTT	3219
OY	889	ACAAA-----TGAACAAGATTACACTATCATATTACTTTAGATCATATTCAAAACGCT	942
Db	3220	ACAAACACGCGCTATGAAAAATGTGAAGTGCAAACACATTTCTGACATTTGTATGCT	3279
OY	943	GATGCACTGTGATCAGTGCATTCCTATGATATACATAATTGGTTACCGAATGCTCCAGGT	1002
Db	3280	GATCATCTCGTGACAGTCGATCTCTTAATGATATATTAATATGTATGACCGGAAGTTTCAGT	3339
OY	1003	ATGAACATATGATATATCAAGACTTTAAAGCAGATCATGCAAGGTATTAATTTATAT	1062
Db	3340	ATGAATTAACGAATCTTATACAGACTTAACACTTCGTTAGAAATGCGTTCTACTCTGAT	3399
OY	1063	GATGACCAAAATGTATCAATCAAAATGTGACTTTTACAGAAGATTACAGAGATGACGCA	1122
Db	3400	GACACAGCGGAATCTGATTAATAATATGGGCGCTTTGCAATGGCGTTATGATATGGCAAGCT	3459
OY	1123	ACAGGAAATGCCCGGCTACAAACAAATGATGAGACCTTCAGTATTAAGTTCTATCAAAATGG	1182
Db	3460	ACCCCGCATGACAGATGAGAGCAAAATATGATATGATCAAGCTGCGTCCGCCAAATTTGG	3519
OY	1183	AGCGCGGGGATGTCAAAATCTGCATGAGCTCAACATATCATATGATATATGTTATGCTGTGT	1242
Db	3520	GATGCAATGTGTGCAACAGCTGTGATGCAACACATGCGGTTATGATATTCGATGTC	3579
OY	1243	ATTGCAAAAAAGAGACCTGAAAAAGGATATGTAACGATGATGAAATTTGTAATGAGAA	1302
Db	3580	ACGGGAGAAAGAAAGATTCGGGAGCCGGCAATGTTACCTTTAGTGACTGACAAATCAT	3639
OY	1303	CAGGAAACATTAAGTTCACTTTCTTGGAGAGAG	1336
Db	3640	GTGACAAAGCTGAGACTTTACTTCTTGGATATAG	3673

RESULT 15
US-11-091-654-17
; Sequence 17, Application US/11091654
; Publication No. US20050172355A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao


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/ APPLICANT: YOKOYAMA, Tomoko
/ APPLICANT: AOYAGI, Motichi
/ APPLICANT: HASEGAWA, Makoto
/ APPLICANT: EHARA, Gaku
/ APPLICANT: KIMURA, Masaharu
/ APPLICANT: NISHIHASHI, Hideji
/ TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
/ TITLE OF INVENTION: Insecticidal effect on scutabaeidae insects and
/ TITLE OF INVENTION: polynucleotide encoding the same
/ FILE REFERENCE: OP135
/ CURRENT APPLICATION NUMBER: US/11/091,654
/ PRIOR FILING DATE: 2005-03-29
/ PRIOR APPLICATION NUMBER: JP 2001-115754
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: JP 2001-203463
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 17
/ LENGTH: 4359
/ TYPE: DNA
/ ORGANISM: Bacillus popilliae
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (250)..(4245)
US-11-091-654-17

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Query Match 18.2%; Score 306.4; DB 10; Length 4359;

Best Local Similarity 55.4%; Pred. No. 8.3e-59;

Matches 817; Conservative 0; Mismatches 516; Indels 141; Gaps 6;

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QY 1 GTGAGTCTATGTTTCAAGTAGTACGAAATAATACCTTAAATAGAAACGACAGATTAT 60
DB 2203 GTGAACCAATTTGTTTACAGATGATCGAAAAAGCCCTAAAGAGACGACCGATTAT 2262
QY 61 GAAATAGATCAAGCGGCGCTTTCTATAGATGATGTCAGTGAACAAATACTCTCGAAA 120
DB 2263 GAGATGATCAAGCGGCGCAACGCTGATGATTGATTCGATG--AGTGTGACATGAG 2319
QY 121 AAAATATGTTATGGGATGAAATAAACTGCGCAAAACCTTAGTCAGTCTCTATCTTA 180
DB 2320 AAAATGATCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2379
QY 181 CTCGAAATGAGACTTTCT-----CGGAATGATTGACA 216
DB 2380 CTCGCTCAATGGGAATTTCCATGATCTATATCCAGCTCTGAGAGGAGAAATCCATGAAA 2439
QY 217 TTCGGTAATGATATTATCAATAGATCCATTAATCCATATTTTAAAGAAATTTCTACAG 276
DB 2440 ACAAGTCCGAATGTTACGATCCGTCAGATTAACCCGATTTTAAAGCCATTAATCTCAGT 2499
QY 277 ATGCGTGAGACAGACATATATGGAAC-----TCTATTTTCAACTATATCTGCA 330
DB 2500 ATGGCGGTGCGCAACATATCCAGGCCAACATGATAGCTTCCCACTGATGCTATCA 2559
QY 331 AAAATGATGAGTCTTAATTTAAACCATATACAGTTATCGAGTAAAGAGGTTTGTGGA 390
DB 2560 AAAATGATGAGACCAATTTAAAGCCATATACAGGTTATAGTGGCGGTTTGTGGC 2619
QY 391 AGTAGTAAGATTGTAATTAATGTAACGTTAGGGAAGAAATTAATGCTATCAG 450
DB 2620 ACACAGAAAGATCTGAGCTGTTGTTACCGCTTAATAGAAAGTGTGATGATTTTA 2679
QY 451 AATGTTCAATGATTTGGCTATATGACGCTTAATCTTCAATGAGAGATTATCCGTGT 510
DB 2680 GATGTACCGGATTAATATCCGCGATGCGCGATCTCTGTGCGGTGAATTTGATGATGC 2739
QY 511 GAATCATCGTC-----TGATATGTGAGCCAAAG----- 539
DB 2740 AAGCCTATTCGATTCACCTTACTTCAGAAATGTAACCTGATGTTTAAATCAGATG 2799
QY 540 ----- 539

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DB 2800 CAACCATCTCTTGGCCACCAATCAGATGTCGATTAACAATACATGAACGAGCAG 2859
QY 540 -----GTATCTTACACCAACAGATGATATGCTCCGATATGATGATGCCG 588
DB 2860 AGTACTACCATGAATCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2919
QY 589 CAAATATGATAGAAAGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 648
DB 2920 AGTGAATTCGCAAAACATCGCAAAATGTCATCAAGCGCATCAATTAAGTTCCAGAT 2979
QY 649 GACACCGGAGAGTGAATACAAATCAATGATGATGATGATGATGATGATGATGATGATG 708
DB 2980 GATACCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3039
QY 709 AATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
DB 3040 GCCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3099
QY 769 GGTGAAGCATTTGGCCATGTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 828
DB 3100 GTCGAAGCTTATGAACCTTGTCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 3159
QY 829 AAACGTTGGGAAACACAAACAGCTATGATCCAGCAAAACAGGCTGTAGATCATATTT 888
DB 3160 CACTGTTCCCAACCAACCAATATGATGATGATGATGATGATGATGATGATGATGATG 3219
QY 889 ACAA-----TGAAACAAGATTACATATCATATTTACTTTAGATCATATTCAAACGCT 942
DB 3220 ACAAAACACGCGTATGAAATTTGAAGTTGCAAAACAAACATTTTGTATGATGCT 3279
QY 943 GATGACGCTGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002
DB 3280 GATCATCTGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3339
QY 1003 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062
DB 3340 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3399
QY 1063 GATGACGAAATGCTATTAACAATGATGATGATGATGATGATGATGATGATGATGAT 1122
DB 3400 GACGACGGAATCTGATTAATAATGATGATGATGATGATGATGATGATGATGATGAT 3459
QY 1123 ACAGAAATGCGCGGTATCAAAATGATGATGATGATGATGATGATGATGATGATGAT 1182
DB 3460 ACCCGCATGACAGATGAGCAAGATGATGATGATGATGATGATGATGATGATGATG 3519
QY 1183 ACAGCGGGGTATCTCAAACTTGCATGCTCAAGATCATCATGATGATGATGATGATG 1242
DB 3520 GATGCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3579
QY 1243 ATTGCCAAAAAGAAAGACCTGGAAGAGGATGATGATGATGATGATGATGATGATGAT 1302
DB 3580 ACAGCGGAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3639
QY 1303 CAGGAAACCTTAAGTCACTTTTCCGGAAGAG 1336
DB 3640 GTGACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3673

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 04:36:51 ; Search time 743 Seconds
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2076.406 Million cell updates/sec

Title: US-10-781-979-6

Perfect score: 1686
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapept 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 12494176

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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12: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384.2	22.8	4359	US-11-091-643-3	Sequence 3, Appl
2	312.8	18.6	4366	US-11-091-643-19	Sequence 17, Appl
3	306.4	18.2	4359	US-11-091-643-17	Sequence 17, Appl
4	302.6	17.9	3621	US-11-058-727-1	Sequence 1, Appl
5	302.6	17.9	3621	US-11-108-389-1	Sequence 1, Appl
6	302.6	17.9	3621	US-11-224-624-1	Sequence 3, Appl
7	302.6	17.9	3633	US-11-058-727-3	Sequence 3, Appl
8	302.6	17.9	3633	US-11-108-389-3	Sequence 3, Appl
9	302.6	17.9	3633	US-11-224-624-3	Sequence 3, Appl
10	302.6	17.9	4874	US-11-058-727-17	Sequence 17, Appl
11	302.6	17.9	4874	US-11-108-389-17	Sequence 17, Appl
12	302.6	17.9	4874	US-11-224-624-17	Sequence 17, Appl
13	302.6	17.9	6613	US-11-058-727-18	Sequence 18, Appl
14	302.6	17.9	6613	US-11-108-389-18	Sequence 18, Appl
15	302.6	17.9	6613	US-11-224-624-18	Sequence 18, Appl
16	302.4	17.9	4188	US-11-091-643-5	Sequence 5, Appl
17	295.2	15.4	4119	US-11-070-575-4	Sequence 4, Appl
18	259.4	15.4	3531	US-11-226-943-9	Sequence 9, Appl
19	259.4	15.4	3531	US-11-226-943-11	Sequence 11, Appl
20	259.4	15.4	3531	US-11-226-943-13	Sequence 13, Appl
21	259.4	15.4	3534	US-11-226-943-25	Sequence 25, Appl

22	259.4	15.4	3534	US-11-226-943-27	Sequence 27, Appl
23	258.8	15.3	3579	US-11-226-943-29	Sequence 29, Appl
24	239.8	14.2	3546	US-10-755-092-27	Sequence 27, Appl
25	238.6	14.2	3534	US-11-226-943-33	Sequence 33, Appl
26	217.4	12.9	3547	US-10-755-092-16	Sequence 16, Appl
27	185	11.0	3468	US-10-755-092-1	Sequence 1, Appl
28	185	11.0	3468	US-10-755-092-8	Sequence 8, Appl
29	167.6	9.9	3546	US-10-755-092-10	Sequence 10, Appl
30	164.2	9.7	3546	US-10-755-092-12	Sequence 12, Appl
31	152.8	9.1	402	US-11-091-643-1	Sequence 1, Appl
32	79.6	4.7	3624	US-10-755-092-6	Sequence 6, Appl
33	68.2	4.0	3546	US-10-755-092-14	Sequence 14, Appl
34	66.6	4.0	3468	US-10-755-092-4	Sequence 4, Appl
35	65	3.9	3468	US-10-755-092-2	Sequence 2, Appl
36	47.4	2.8	3143	US-11-165-819-9	Sequence 9, Appl
37	47.4	2.8	3143	US-11-165-819-29	Sequence 29, Appl
38	44.4	2.6	201	US-11-124-3674-26061	Sequence 26061, A
39	44	2.6	1811	US-11-049-348-2	Sequence 554, App
40	42.8	2.5	7023	US-11-052-554A-554	Sequence 71, Appl
41	42.6	2.5	8607	US-10-240-708-71	Sequence 9, Appl
42	42.2	2.5	1065	US-11-189-817-1	Sequence 5869, Ap
43	42	2.5	200	US-11-098-686-5869	Sequence 9606, Ap
44	42	2.5	3309	US-11-098-686-9606	Sequence 8739, Ap
45	42	2.5	1457619	US-11-098-686-8739	

ALIGNMENTS

RESULT 1				
US-11-091-643-3				
Sequence 3, Application US/11091643				
Publication No. US20050246789A1				
GENERAL INFORMATION:				
APPLICANT: TANAKA, Masao				
APPLICANT: YOKOYAMA, Tomoko				
APPLICANT: AOYAGI, Moriochi				
APPLICANT: HASEGAWA, Makoto				
APPLICANT: EHARA, Gaku				
APPLICANT: KIMURA, Masaharu				
APPLICANT: NISHIHASHI, Hideji				
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or				
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and				
TITLE OF INVENTION: poynuclotide encoding the same				
FILE REFERENCE: OP1335				
CURRENT APPLICATION NUMBER: US/11/091,643				
CURRENT FILING DATE: 2005-03-29				
PRIOR APPLICATION NUMBER: JP 2001-115754				
PRIOR FILING DATE: 2001-04-13				
PRIOR APPLICATION NUMBER: JP 2001-203463				
PRIOR FILING DATE: 2001-07-04				
NUMBER OF SEQ ID NOS: 22				
SOFTWARE: PatentIn Ver. 2.0				
SEQ ID NO 3				
LENGTH: 4359				
TYPE: DNA				
ORGANISM: Bacillus popilliae				
FEATURE:				
NAME/KEY: CDS				
LOCATION: (282)..(4229)				
US-11-091-643-3				
Qy	1	GTGAGTCCTATGTTTACAGTAGTACGAAAAATACGTTAAAAATATGAAAGACAGATTAT	22.8%;	Score 384.2; DB 10; Length 4359;
		Best Local Similarity 58.0%;	Pred. No. 2.7e-76;	
Db	2337	GTGAAACATTGTTTACAGATGATGAAAAAGCGCTTAAAAAGAAAGCAGACCGATTAT	0; Mismatches 528; Indels 54; Gaps 5;	
		Matches 805; Conservative		
Oy	61	GAATATGATCAAGCGGCATTTCTATATGAAATGTATGTCAATGAACAAATCCCTCAGAA	120	
Db	2397	GAGATTCATCAAGCGGCAACGTGTGATTTATATCGATG--AGTGTGACATGAG	2453	

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Qy 121 AAAATATGTTATGGAGTAAATAAACTGGGAAAACAATTAGCTCTGTATCTA 180
Db 2454 AAAATGATCTGTATGATGAATAAATATGCAAAACAATCAGCCGCAATTTA 2513
Qy 181 CTCGAAAATGAGACTTTTCT-----GGGAATGATTGACA 216
Db 2514 CTGCTCAATGGGAATTTGATGATCTATATCCAGCTCGAAGAGGAAATCCATGAAA 2573
Qy 217 TTCGTAATGATATATATCATAGATCCAAATATCTATTTTAAAGAAAATTTCTACAG 276
Db 2574 ACAAGTCGCGATGTATACATCCGTCAAGATAACCCGATTTTAAAGGCATATCTCAGT 2633
Qy 277 ATGGGTGAGACAGACATATATGGAAC-----TCATTTCCAACTATATCTGTCAA 330
Db 2634 ATGGCGGTGCAACGATATATGAGGCCAACATGATACCTTCCCACTATGTATATCA 2693
Qy 331 AAAATAGATGATCTAAATTAATAAACATATACAGTTATCGAGTAAGAGGTTTGTGGA 390
Db 2694 AAAATAGACGAAGCCAAATTAAGCCATATACAGGTATTAAGTCCGGGTTTGTGTGT 2753
Qy 391 AGTAGTAAGATTGAAATTAATGTTAAACGTTACGGGAAAGAAATGATGCTATCTATG 450
Db 2754 AGCAGCAAAAGCTTAGAGCTGTGGTTACAGCTATTAATGAAGAAGTCGATGCGATTTTA 2813
Qy 451 AATGTTCCAAATGATTTGGCCATATATGAGGCTAATCTTCATGTGAGATTTATGCGTGT 510
Db 2814 GATTTACCGGATTAATATCCCGATGCGCCGACCTCTGTCTGGGTGAAATTTGATGATGC 2873
Qy 511 GAATCATCGTC-----TCAGTATGAGCCAAAGGGTATCTTACACCAACA 555
Db 2874 AAGCCATATGTGATTCACCTTTACTTCAGAAATGTAACCGTAGTTTAATCAGATG 2933
Qy 556 GATGATATGCTCCCGATATGTATGATGATGCGGCAAAATATATGATGAAGAGCTGTAAG 615
Db 2934 CAACCATCTCTTGGCCACACATCAGATGATGTCGATTAATACAGAAAACACCGCAAA 2993
Qy 616 TGTACAGATGCTATCCATTTGATTTGATATATGACCGGAGAAAGTATGATCAAAATCA 675
Db 2994 TGTCTACAGGCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3053
Qy 676 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 735
Db 3054 GATTTGGCATTTGGGTGATCTTCAAAATCTGTGCAAGATGTTAGCAAGCTTAATAT 3113
Qy 736 AATCTGAAGTCAATTGAAGAAAGACCACTAACAGTGAAGCAATTTGGCAATGTGAACAA 795
Db 3114 GATTTGGAAGTGAATGAAGAAAGAGCGCTGGGTGTCGAAGCATTTGTCAMAGAAA 3173
Qy 796 AAGGAAAAGAAATGGAACCAACATGGAAGAAAACGTTGGGAAAACAACAAGCCTAT 855
Db 3174 AGAAGAAAAGAAATGGAACCAACATGGAAGAGCACTGTGTGCAACCAACAACAATAT 3233
Qy 856 GATCAGCAAAAACAGGCTGTATGATGATTTTACAA-----TGAACAAGTTACAC 909
Db 3234 GATCGGGCAAAACAGCGGTGATGCGTTATTCACAAACAGCGCTATGAAAATATGAAG 3293
Qy 910 TATCATATTTACTTTAGATCATATTTCAAAACGCTGATGCACTGTGATCGATTTCCCTAT 969
Db 3294 TTCGAAACCAACCATCTCCAAATATTTTGTATGTCATCTGTGCAATTCATTCCTTAT 3353
Qy 970 GTATACCTTAATTTGTTATGCGAATGCTCAGGTAAGAACTATGATGTATATCAAGATTA 1029
Db 3354 GTATATATTAATATATGACCGGAAGTTCAGGTATGAATTAAGAACTTATACAGAGCTA 3413
Qy 1030 AACGACGATATCATGCAAGGTTATTAATTTATATGATGACGAATGTCTAATCAATGAT 1089
Db 3414 AACACTCTGTTCAAGATGCGTTCTATCTATATATGACGCGGAATCTGATTAATAATGGG 3473
Qy 1090 GACTTTACACAAGATTACAGGATGCGACGCAAGAAATGCCGCGGTACACAATATG 1149
Db 3474 CGCTTTAGCAATGGGCTTATGTATTTGGCAGGCTACCCGCAATGCAAGATGGAACAAAGA 3533

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Qy 1150 GATGAGCTTCAGTATTAGTTCTTATCAAAATTTGAGCGCGGGGTATCTCAAAACTTCAT 1209
Db 3534 TATGAAATATCTGTACTGTCTGCTGCCAAATTTGGATGCAATGTGTGCGAAAGATCTTGT 3593
Qy 1210 GCTCAAGATCATCATGATATATGTTTACGTGTGATTTGCCAAAAAAGAGACCTTGAAAA 1269
Db 3594 ATGACACCAATCGCGGTATATGTATGTCGTGTCAAGCGGCAAGAAAAGAAATCCGGAGCT 3653
Qy 1270 GGGTATGTAAGATGATGATTTGTAATGGAAGAGAAACACTTAAGTTCACTTCTTGC 1329
Db 3654 GGCATGTATACCTTCACTGACTGTGCAACCAATGTGCAACAAAGCTTACTTCTTGC 3713
Qy 1330 GAAGAAG 1336
Db 3714 GATATAG 3720

RESULT 2
US-11-091-643-19
; Sequence 19, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Morichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabeidae insects and
; FILE REFERENCE: OP1335
; CURRENT APPLICATION NUMBER: US/11/091,643
; PRIOR FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 4366
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-11-091-643-19

Query Match 18.6%; Score 312.8; DB 10; Length 4366;
Best Local Similarity 55.7%; Pred. No. 2e-60;
Matches 821; Conservative 0; Mismatches 512; Indels 141; Gaps 6;

Qy 1 GTGAGCTCTATGTTTACAGTAGTACGAAAAATACGTTAAATAATAGAAAGACAGATTTAT 60
Db 2213 GTGAACATTTGTTTACAGATGATCGAAAAAGCGCTAAAGAAAGACAGACGATTTAT 2272
Qy 61 GAAATAGATCAAGCGGCCATTTCTATAGAAATGTAATGTCAAGTGAACAAATCTTCAGGA 120
Db 2273 GAGATTATCAAGCGGCCCAAGTGTAGATTTGATATCGGATG---AGTGTGACATGAT 2329
Qy 121 AAAATATGTTATGAGTGAATAAATCTGCAAAACAACCTTAGTCACTGTCTGTATCTA 180
Db 2330 AAAATGATCTGTATGATGAAGTAATAATGCAAAACAACCTACGCCAAGCCGCAATTTA 2389
Qy 181 CTCGAAAATGAGACTTTTCT-----GGGAATGATTGACA 216
Db 2390 CTGCTCAATGGGAATTTGATGATCTATATTTCAAGCTCGAAGAGGAAATCCATGAAA 2449
Qy 217 TTCGTAATGATATATATCATAGATCCAAATATCTATTTTAAAGAAAATTTCTACAG 276
Db 2450 ACAAGTCGAGATGTATGATGATCGCAAGATTAACCGATTTTAAAGCCATATATCTCAGT 2509

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OY 277 ATGCGTGAGCAGCAGCATATATGGAAC-----TCTATTTCCAACCTATATCTGTCAA 330
DB 2510 ATGGGGGTGGCGAAGCATATCGAGGCCACCAATGATACCTTCCCAAGATCTCTATCA 2569
OY 331 AAAATAGATGAGTCAAAATTAAACCATATACGTTATCGAGTAAGAGGGTTGTGGGA 390
DB 2570 AAAATAGACGAAGCCAAATTAAAGCGTATACAGTTATTAAGTCGGGGTTGTGGC 2629
OY 391 AGTAGTAAGATTTGAAATTAATGTGTAACAGCTTACGGGAAAGAAATGATGCTATCATG 450
DB 2630 AGCAGCAAAAGCTCTAGAGCTGTGTGTTACAGCTTATATGAAGAGTTGATGCGATTTTA 2689
OY 451 AATGTTCCAATGATTTGGCTTATATGCAAGCTTAATCCTTCAATGTGAGATTAATGCTGT 510
DB 2690 GATGTACCGGATTAATATCCCGCATCGCCGACTCTGTCTGTGGGTAATTTGATGATGTC 2749
OY 511 GAATGATGTC-----TCAGTATGTGAGCCAAAG----- 539
DB 2750 AAGCCCTATTGCTATCCACCTTTACTTCCAGAAATGTAACCTTGAGTTTATAATCAGATG 2809
OY 540 ----- 539
DB 2810 CAACCATCTCTTGGCAACCAATGAGATGTCATTAACATTAACATGAACGAGCAGC 2869
OY 540 -----GTATCTTACACCAACAGATGATATGCTCCCGATATGTATGCAATGCCG 588
DB 2870 AGTACTACCATGATATCTTGCATGATATCTCCCTTACCCCTGAATATGATCAGCCCA 2929
OY 589 CAAATATATGATAGAAAGATGTAAGTGTGACGATCGTCAATTCATTTGATTTTATAT 648
DB 2930 AGTGAATTCGGCAAAACATGCAAAATGTCATCAAGCCATCAATTTGATTTCCAT 2989
OY 649 GACACCGGAGATGATCAAAATCAAAATGATGATGATGATGATGATGATGATGATGAT 708
DB 2990 GATACCGGAGCATGATTTGTCGAAGATTTGGGATTTGGGATCTTCAAAATCTGT 3049
OY 709 AATCCAGATGATAGCTTACAGTAGGAATCTTAAGATCATTTGAAGAGCAACTAC 768
DB 3050 GCCACAGATGATAGCAGCAAGCTTAAATGATCTGAAGTATTTGAAGAGAGCGCTG 3109
OY 769 GGTGAAGATTTGGCATGCTGTAACAAAAGAAAGAAATGGAACCAACATGAGAA 828
DB 3110 GTCGAAGATTTGAACCTTGTCAAAAAGAAAGAAATGGAACATGAGAGAGCAG 3169
OY 829 AAACCTTGGGAAACCAACAGCTTATGTCAGCAAAACAGCTGATGATGATGAT 888
DB 3170 CACTGTTCGCAAAACCAACCAATATGATGCGGCCAAACATGCGGTATGCGTTAT 3229
OY 889 ACAAAATGAAC-----AAGAGTTTACATATATTTCTTTAGATCATATCAAAACGCT 942
DB 3230 ACAAAACAGCGCTATGAAATTTGAAGTTTGAACCAACATTTCTGACATTTTGTATGCT 3289
OY 943 GATGACGTGATCAGTCCGATTTCCCTATGATACATTAATTTGTTACCGGAATGCTCCAGCT 1002
DB 3290 GATCATCTCTGTCAGTCTTCTTATGATATTAATTAATTAATGATGATGATGATGAT 3349
OY 1003 ATGAATATGATGATATCAAGAGTTTAAACGACGATCATGCAAGTTATATTTATAT 1062
DB 3350 ATGAATATGAACTCTATTCAGAGCTTAACACATGCTTCAAAATGCGTTTACCTGTAT 3409
OY 1063 GATGACGAATATGATCAAAATGATGATCTTTTACCAAGATTTACAGGAGTGGCAGCA 1122
DB 3410 GACCAAGCGGAATCTGATTTAAATGAGCGCTTTAGCAATGAGCTTATGATTTGGCAG 3469
OY 1123 ACAGAAATATGCGCGGTATCAAAATGATGATGATGATGATGATGATGATGATGAT 1182
DB 3470 ACTCTCATGCAAGATGAGCAAGAAATGAGAAATGCGTCTCTGTCTGCGCAAAATG 3529
OY 1183 AGCGGCGGGTATCTCAAAATTTGATGCTCAAGATCATGATGATGATGATGATGATG 1242
DB 3530 GATGCAATGCTGCGAAGATCTTTGTATCGAAACAAATCGCGTTATGATTTGCGTGT 3589
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OY 1243 ATTGCCAAAAGAGACCTGGAAAGGATATGAAAGATGATGATGATGATGATGATG 1302
DB 3530 AGCGGAGAAAAGAGATCCGGAGCTGCGCAATGTTACTTTAGTACTGTGAATAATCAT 3649
OY 1303 CAGGAACACTTAAGTCACTTCTTGGCAAGAG 1336
DB 3650 GTGCAACAGTGAAGCTTTACTTTTGGATATAG 3683

RESULT 3
US-11-091-643-17
; Sequence 17, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OP1335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (250) .. (4245)
US-11-091-643-17

Query Match 18.2%; Score 306.4; DB 10; Length 4359;
Best Local Similarity 55.4%; Pred. No. 5,4e-59;
Matches 817; Conservative 0; Mismatches 516; Indels 141; Gaps 6;

OY 1 GTGAGTCCATGTTTACAAAGTAGTACGAAATATGATGATGATGATGATGATGATGAT 60
DB 2203 GTGAACCATTTTGTATACGATGATGATGATGATGATGATGATGATGATGATGAT 2262
OY 61 GAATATGATCAAGCGGCAATTTCTATAGATGATGATGATGATGATGATGATGATGAT 120
DB 2263 GAGATTTGATCAAGCGGCAAGTGTATGATGATGATGATGATGATGATGATGATGAT 2319
OY 121 AAAATATGATTTGAGATGAAATTAACCTGCGAAACCACTTAAGTCACTGCTGATCT 180
DB 2330 AAAATATGATCTGTTGATGAAATTAATGCAAACTAGCCAGCCGCAATTTTA 2379
OY 181 CTCGAAATGAGACCTTTCT-----GGGATGATTGAGCA 216
DB 2380 CTGCTCAATGGGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2439
OY 217 TTGCGTAAATGATATTTATCAATAGATCAATAATCTTATTTTAAAGAAATTTCTACAG 276
DB 2440 ACAAGTCGAATGTTATACGATCGTCAAGTAAACCGAATTTTAAAGCCATATCTCAGT 2499
OY 277 ATGCGTGAGCAGCAGCATATATGGAAC-----TCTATTTCCAACCTATATCTGTCAA 330
DB 2500 ATGGGGGTGGCGAAGCATATCGAGGCCACCAATGATACCTTCCCAAGATCTCTATCA 2559
OY 331 AAAATAGATGAGTCAAAATTAAACCATATACGTTATGAGTAAAGAGGGTTGTGGGA 390
DB 2560 AAAATAGATGAGCCAAATTTAAAGCATATACAGGTATTAAGTCCGCGGTTGTGTGGC 2619
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QY 391 AGTAAAGATTGAAATTAATGTAACAGCTTACGGGAAGAAATGATGCTATCATG 450
DB 2620 AGCAGCAAGATCTGAGAGCTGTGGTTACACCTTAATGAAGAGTTGATCGATTTTA 2679
QY 451 AATGTTCCAAATGATTTGGCCCTATATGACGCTTAATCCTTCATGTGAGATTATCGCTGT 510
DB 2680 GATGATACGGGAATATATCCCGATGCGCGACTCTGTCTGTGGGGTAATTTGATGATGTC 2739
QY 511 GAATCATGTC-----TCAGTATGTAGCCCAAG----- 539
DB 2740 AAGCCCTATCGTATCACTTTACTTCCAGATGTAAACCTGAGTTTAAATGAGATG 2799
QY 540 ----- 539
DB 2800 CAACCATCTCTTGGCACCACATCATGATGTCGATTACATAATACATGAACGAGCACG 2859
QY 540 -----GTATCTTACACCAACAGATGATATGCTCCGATATGATGATGATGCGCG 588
DB 2860 AGTACTACATGAAATCTTAGCATGAAATCCTCCCTTACGCTGAATAGCATCCAGCCAA 2919
QY 589 CAAAATATAGATGAAGAGATGTGAAGTGTACGATTCGTATCCATTTGATTTTCAATTT 648
DB 2920 AGTGAATTCGCGAGAAAACATGCAAAATGTCAAGCGCATCAATTTGAGTTCCACATTT 2979
QY 649 GACACCGGAGAGTAGATACAAATACAAATGATGATTTGATGCTTATTTAAATTTCT 708
DB 2980 GATACCGGAGACATGATGATTTGTGTGAAGATTTGGGCATTTGGGTATCTTCAAAATCTGT 3039
QY 709 AATCCAGATGATACGCTTACAGTAGAGAACTTGAAGTCAATTTGAAGAAAGACACATAACA 768
DB 3040 GCCACAGATGATACGCAAGCTTATGATCTGAAAGTATTTGAAGAAAGAGCGCTGGGG 3099
QY 769 GGTGAAGATTTGGCATGTGTAAACAAAAGAAAGAAATGAAACAAACATGTGAGAAA 828
DB 3100 GTCGAAGCTTATGAACTTGTCAAGAAAAGAAAAGAAATGAGACATCAGAAAGAGAGAG 3159
QY 829 AAACGTTGGGAAACCAACAGCCTATGATCCAGCAAAAGCGGTGATGATCATTTATTT 888
DB 3160 CACTGTTGCCAATACCAACAAATATATGTCGCGCAACATGCGGTATGAGCGCTTATTT 3219
QY 889 ACAAA-----TGAAACAAGATTACATATCATATTTAGATCATATTTCAAAACGCT 942
DB 3220 ACAAAACAGCGCTATGAAAAATTTGAAGTTGAAAACACATTTCTGACATTTTGTATGCT 3279
QY 943 GATGACCTGTGATCATGCTGATTTCCCTATGTATACCAATTTGTTTCCGATGCTCCAGGT 1002
DB 3280 GATCATCTCGTGACATGCTTCTTATGTATTAATAATATGATACCGAAGTTTCAGGT 3339
QY 1003 ATGAATGATGATGTATCAAGATTAAACGAGATATCATGCAAGTTATTAATTTAT 1062
DB 3340 ATGAATTCAGAACTTATACAGAGCTTAAACATCTCGTTACAGATGCGTTTCACTGTAT 3399
QY 1063 GATGACGAAATGTCTATTAACAATGATGATCTTTACACAAGATTTACAGGATGACGCA 1122
DB 3400 GACCAAGCGGAATCTGATTTAAAAATGGGCGCTTTACATAGGGCTTATATGGAACGT 3459
QY 1123 ACAGAAATGCGCGCGGTACACAAATGATGAGCTTCAATTTATTTGTTTCAATTTGG 1182
DB 3460 ACCCGCATGACGAGTGAGCAAAATATGATGATGATGCTGCTGCGAATTTGG 3519
QY 1183 AGCGCGGGGATATCTCAAAACCTTGATGCTCAAGATCATGATGATGTTAGATGCTG 1242
DB 3520 GATGCAATGTGTGCGAACAGCTGTGTATTCGAACCAATCGGCTTATGATTTGGGTGTC 3579
QY 1243 ATTGCAAAAAAGAGAGCTGGAAGAGGATATGTAACATGATGATTTGTAATGGAAG 1302
DB 3580 ACGGGAAGAAAAGAGATCCGGAGCCGGAATGTTACTTTAGTACGTGTGCAAAATCAT 3639
QY 1303 CAGGAAACATTAATGTTCACTTTCTTGGGAGAG 1336
DB 3640 GTCGACAGCTGAGCTTACTTTCTTGGATATAG 3673

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RESULT 4
US-11-058-727-1
; Sequence 1, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Prensail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Peestical
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12Ib-1
US-11-058-727-1

Query Match 17.9%; Score 302.6; DB 11; Length 3621;
Best Local Similarity 55.4%; Pred. No. 3.7e-58;
Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;
QY 22 AGTACGAAATTAATGAAATGAAACGACGATTTATGAAATGATCAAGCGGCATT 81
DB 2053 AATCAAAAGATGCTTACGACCGGCTAACGATTAAGAAATCAAGCGGCAAAAC 2112
QY 82 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
DB 2113 TTATGAAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2112
QY 142 ATAAATGCGCAAAACAACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 197
DB 2173 GTGAGAGGGAAGAAACCGCTTACGAGCAAGTAAATTTGCTTCAAGATTTCCAA 2232
QY 198 -----TTTGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
DB 2233 GAGTAAATGAGAAATTTGCTGAGCGCAAGTACGGAATTTGATTAAGAAAGGGAT 2292
QY 250 CTTATTTTAAAGAAATTTCTACAGATGCGTGGAGCAGAGCATATATGAAATCTTA 309
DB 2293 GCTTATTTCAAGGCGCTTATCTACGCTTACAGATGCGAGAGAAATGATACGAAACG 2352
QY 310 TTTTCAACCTATATCTGTCAAAATTAATGATGATGATGATGATGATGATGATGATGAT 369
DB 2253 TATCAACGATATCTGTATCAAAATTAATGATGATGATGATGATGATGATGATGATGAT 2412
QY 370 CGATTAAGAGGCTTTGGGGAAGTAAAGATTTGAAATTAATGATGATGATGATGATGAT 429
DB 2413 AGATTGAGAGGCTTTGGGGAAGTAAAGATTTGAAATTAATGATGATGATGATGATGATGAT 2468

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QY 430 AAAGAAATGATGCTATCATGAAATGTTCCAAATGATTTGGCTATATGACGCTAATCCT 489
Db 2469 -----l-TCAACGACCAACGGAATTTGAAAAATGACCGGATGATTTGGTCCAGATGTA 2520
QY 490 TCATGAGAGATTTATCGCTGATCATGCTCTCAGTATGTGAGCCAAAGGATATCCTTACA 549
Db 2521 TCTCTGTTAACTCGGATGCTAGT-----A 2545
QY 550 CCACACAGATGATATGCTCCCGATATGTATGATGATCCCGCAAAATATGATAGAAAGCAT 609
Db 2546 TCAATCGATGACGCAACAAAGATATGTGAATAGCCGTTTAGAAGTAAACCGTTCTG 2605
QY 610 GTGAAGTGCAGATCGTCATCTTGAATTTTCATATTTGACACCGGAGAAATATATACA 669
Db 2606 GTGAAGCG-----CATGAGTTCTCTATTTCTATTTGATGATGAGGTAATTCATTAAC 2655
QY 670 AATACAAAATGATGATGATGCTTAAATTTTAAATTTTCTAATCCAGATGATGATACCTACA 729
Db 2656 AATGAAATGACGAGAAATATGAGTTGATTTAGATTTAGATTCAGAACCCAGAGGATATGCAACA 2715
QY 730 GTAGGAAATCTAGAAATCAATGAGAGGACCACTAACAGGTGAACATTTGGCAGATGTG 789
Db 2716 CTCGAAACCTTAGAATTTGGTTCAGAGGAGCCTTTATCAGAGACGCAATTAGAACGCTTG 2775
QY 790 AAACAAAAGAAAAGAAATGAAACAAACATGAGAGAAAAACGTTGGGAAACACACAA 849
Db 2776 CAAGAAGAAAGAACACAGTGAAGATTCAAATGACAAAGAGACGTAAGAAACAGATAGA 2835
QY 850 GCGTATGATCCAGCAAAACAGGCTGTAGATGATTTAATTTAACAATGAACAAGTTTAC 909
Db 2836 AGGTATATGCAATCGAAACAGCGGATGAGTCTTATATATGCGGATTTATGAGATCAGCAA 2895
QY 910 TATCATATTTACTTTTGA-----TCATATTCAAAAACGCTGATGCACTGTGATACGTGAT 963
Db 2896 CTGATTCCTGATGTAGATTAAGATTAAGATCTTACGCGGCGCCAAAGTCTGATACGTCAAT 2955
QY 964 CCGTATGATACCAATATTTGTTTACCGAATGCTCCAGGTATGATATGATATGATATCA 1023
Db 2956 CCGTATGATATATACAAATGTTTCCAGAAATACAGGAGATGAATCTATCGAAGTTTACA 3015
QY 1024 GAGTTAAACGAGATATCATGAGAGGTTAATTTATATATGACAGAAATGTCATACA 1083
Db 3016 GAATTAACAGATGACTCCAAACAGGTGAGAGTTGTATGATCAGGAAATGCTATACA 3075
QY 1084 AATGATGATTTTACCAAGATTTACAGGATGSCACGCAACAGAAATCCGCGGTACA 1143
Db 3076 AATGATGATTTTGAATGAGTTAAGTATATGGAATGCAACCGCTGAGTAAAGTACA 3135
QY 1144 CAAATGATGAGCTTCAATTTAATTTAGTTCTATCAATTTGAGCGGCGGTTATCTCAAAC 1203
Db 3136 CAAATCAATCATACATCTGCTCTTGATTTCCAACTGGGATGAGCAAGTTTCGCAACAG 3195
QY 1204 TTGCAATGCTCAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
Db 3196 TTACAGTTCAACCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3255
QY 1264 GGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
Db 3256 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3315
QY 1324 TCTTGGAGAGAG 1336
Db 3316 GCAAGCATTAAG 3328

```

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; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cys1218-1
US-11-108-389-1

Query Match 17.9%; Score 302.6; DB 11; Length 3621;
Best Local Similarity 55.4%; Pred. No. 3.7e-58;
Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;

QY 22 AGTAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 81
Db 2053 AATACAAAAGATGCTTACGACACGAGCGTACGATGATGATGATGATGATGATGATGAT 2112
QY 82 TCTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
Db 2113 TTAGTGAATGCTTATCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2172
QY 142 ATAAACGCGCAAAACCTTAGTCACTGCTGATATCTTCAATTAATGAGACTT----- 197
Db 2173 GTGAGAGAGGCAAAACGCTCAGTGAAGCAGTAAATTTGCTTCAAGATCCAGATTTCCA 2232
QY 198 -----TTCTGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
Db 2233 GAGATTAATGAGAAATGCTGACGCGCAAGTACGGAATTTGAGTTATGAGAGGAT 2292
QY 250 CCTATTTTAAAGAAATTTCTACAGATGCTGAGACGAGACATATATGAACTCTA 309
Db 2293 GCTTTATTTCAAGGCGCTTATTTACGCTTACAGGTGAGAGAAATGATACGAAACG 2352
QY 310 TTTCAACCTATATCTGTCAAAATTAAGATGATGATGATGATGATGATGATGATGATGAT 369
Db 2353 TATCAAGATATCTGTATCAAAATTAAGATGATGATGATGATGATGATGATGATGATGAT 2412
QY 370 CGAGTAAGAGGTTTGTGGAAGTAAAGTTTGAATTTGAATTTAGTAAACAGTTACGGG 429
Db 2413 AGATTGAGGAGGTTTGTGGAAGGAGTCAAGGATGGAATTTTCAATTTGTCA----- 2468
QY 430 AAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489
Db 2469 -----TCAACGACCAACGGAATTTGAAAAATGACCGGATGATTTGGTCCAGATGTA 2520
QY 490 TCATGAGAGATTTATCGCTGATCATGCTCTCAGTATGTGAGCCAAAGGATATCCTTACA 549
Db 2521 TCTCTGTTAACTCGGATGCTAGT-----A 2545
QY 550 CCACACAGATGATATGCTCCCGATATGTATGATGATCCCGCAAAATATGATAGAAAGCAT 609

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Db 2546 TCATCGATGCGAGCGAACAAGATGTAATGCCGTTTATAGAGTAAAGAAACCGTCTG 2605
Qy 610 GTGAAGTGCACGATGCTATCATTGATTTTCAATATTGACACCGGAGATGATAC 669
Db 2606 GTGAAGCG-----CATGAGTCTCTATATCCATATGATACAGGTAAATTCATTAC 2655
Qy 670 AATAAATATGATGATGATGATGCTTATTAATAAATTTTCAATCCAGATGATACCTCA 729
Db 2656 AATGAATATGACGAATATGCTGATGATTAAGATTACGACCCAGAGGATATGACACA 2715
Qy 720 GTAGGAAATCTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 789
Db 2716 CTCGGAACCTTAGAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2775
Qy 790 AAACAAAGAAAGAAAGATGAAACACATGAGAAAGAAAGAAAGAAAGAAAGAAAGAA 849
Db 2776 CAAGAAGAAAGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAA 2835
Qy 850 GCTTATGATCCGAAACGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 909
Db 2836 AGGTATATGCGATCGAAACAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 2895
Qy 910 TATCATATTACTTTAGA-----TCATATTCAAAACGCTGATGATGATGATGATGAT 963
Db 2896 CTGAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2955
Qy 964 CCTTATGATATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023
Db 2956 CCTTATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3015
Qy 1024 GAGTTAAACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
Db 3016 GAATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3075
Qy 1084 AATGATGATTTTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
Db 3076 AATGATGATTTTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3135
Qy 1144 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
Db 3136 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3195
Qy 1204 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
Db 3196 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3255
Qy 1264 GGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
Db 3256 GGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3315
Qy 1324 TCTTCCGAAGAAG 1336
Db 3316 GCAACGATATATG 3328

RESULT 6
US-11-224-624-1
; Sequence 1, Application US/11224624
; Publication No. US2006021096A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Andre
; APPLICANT: Dong, Hua
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Rice, Janet
; APPLICANT: Schepers, Eric
; APPLICANT: Wong, James
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/297402
; CURRENT APPLICATION NUMBER: US/11/224,624

; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/746,914
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Cyt1218-1
US-11-224-624-1
Query Match 17.9%; Score 302.6; DB 11; Length 3621;
Best Local Similarity 55.4%; Pred. No. 3,7e-58;
Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;
Qy 22 AGTACGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 81
Db 2053 AATACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2112
Qy 82 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
Db 2113 TTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2172
Qy 142 ATAAACATGCGAAACAACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 197
Db 2173 GTGAGAGGCGAAACCGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 2232
Qy 198 -----TTCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
Db 2233 GAGATTAATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2292
Qy 250 CCTATTTTAAAGAAATTTCTACAGATGATGATGATGATGATGATGATGATGATGATGAT 309
Db 2293 GCTTATTTCAAGGCGTTATCTAGGCTTACAGGTCGAGAGAAATGATGATGATGATGAT 2352
Qy 310 TTTCAACCTTATCTGTCGAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 369
Db 2353 TATCCAGTATCTGTCGTCGAAATATGATGATGATGATGATGATGATGATGATGATGAT 2412
Qy 370 CGAGTAAGAGGTTTGTGGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 429
Db 2413 AGATTGAGAGGTTTGTGGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2468
Qy 430 AAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489
Db 2469 -----TCAAAGAAACGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Qy 490 TCAATGGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
Db 2521 TCTCTGTTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2545
Qy 550 CCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
Db 2546 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2605
Qy 610 GTGAAGTGCACGATGCTATCATTGATGATGATGATGATGATGATGATGATGATGATGAT 669
Db 2606 GTGAAGCG-----CATGAGTCTCTATATCCATATGATACAGGTAAATTCATTAC 2655
Qy 670 AATAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729


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Db      2788 CAAAGAGAAACAAGTGAAGATTCMAATGACAGAAGAGCTGAAGAAACAGATAGA 2847
Qy      850 GCCTTGTATCCAGCAAAACAGCCTGTATGATGATTTATTAACAAATGAACAGAGTTACAC 909
Db      2848 AGTATATGCGATCCAAACAAACGGGTAGATCGTTATATATGCGGATATCAGATCAGACA 2907
Qy      910 TATCATATTACTTTAGA-----TCATATTCAAAACGTCATCGACTGTCAGTCGATT 963
Db      2908 CTGAATCCGTGATGTAGATTTACAGATCTTACTGGGCCCCAAGATCTGATACAGTCATT 2967
Qy      964 CCCATATGATACCATATTTGTTTACCAGAAAGCTCCAGGTATGACTATGATATATCA 1023
Db      2968 CCTTACGATATATAAGAAATGTTCCAGAAATACAGAGGATGAACTATACGAAGTTTACA 3027
Qy      1024 GAGTTAAACGCGATATCATGCAAGGTATATATTTATATGATGCAAGAAATGTCATACA 1083
Db      3028 GAATTAACAGATGACTCCACACAGCTGAGAGTTTGTATGATCAGCGAAATCCATACCA 3087
Qy      1084 AATGTGACTTTACCAAGATTTACAGGGATGCGACGCAACAGAAATGCCGCGTACAA 1143
Db      3088 AATGTGATTTTCGAAATGGGTTTAAGTATTTGAAATGCAACCCCTGGCTGAGAAATCAA 3147
Qy      1144 CAAATGATGAGCTTCAGTATTAAGTTCTATCAAAATGGAGCGCGGGTATCTCAAAAC 1203
Db      3148 CAAATCAATCATACATCTGTCTGTGATTCCAAACCTGGAGTACCAAGTTTCGCAACAG 3207
Qy      1204 TTGCATGCTCAAGATCATCATGATATATGTTTACGTTGATTTGCCAAAANAGAGACT 1263
Db      3208 TTTACAGTTCAACCGAATCAAGATATGTTTACAGATTCGCAAGAAAGAGGGGTA 3267
Qy      1264 GAAAAGGGTATGATACGATGATGATTTGATGTAATGAAAAGCAGAAACACTTAAGTTCACT 1323
Db      3268 GGAATGATATATGTAAGTATCCGTATGTGTGAATTCAAACGAAACGTTACTTTTACT 3327
Qy      1324 TCTTCCGAAGAG 1336
Db      3328 GCACGCGATTAATG 3340

RESULT 8
US-11-108-389-3
; Sequence 3, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT FILING DATE: 2005-04-18
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
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; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Cyt1218-2
US-11-108-389-3

Query Match      17.9%; Score 302.6; DB 11; Length 3633;
Best Local Similarity 55.4%; Pred. No. 3.7e-58;
Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;

Qy      22 AGTACGAAAATACGTTAAAAATGAAAACGACAGATTTATGAAATAGATCAAGCGGCATT 81
Db      2065 AATACAAAAGATGGCTTACGACCGAGGCTAAACGATATATGAAATGAAACGCGCAAC 2124
Qy      82 TCTATGAAATGATGATGATGAAACAAATCTCAGAAAAAATATGTTATGGAGTAA 141
Db      2125 TTAGGAAATCTCATGAGATGATTTGTATCAAAATGAAACGATTTATTTGATGCA 2184
Qy      142 ATAAACTGCGAAAACAACTTATGACGTCTGTAATCTACTCAAAATGAGACTT---- 197
Db      2185 GTGAGAGCGAAAACCGCTCAGTGAAGCACTAAATTTGCTTCAAGATCCGATTTCCAA 2244
Qy      198 -----TCTGGAATGATTTGACATTCGCTAATGATATATCATGATTCCAATAT 249
Db      2245 GAGATTAATGAGAAAATGGCTGACGCAAGTACGGGAATGAGTTATGAAAGGGAT 2304
Qy      250 CCTATTTTAAAGAAAATTTCTACAGATGCTGAGACAGAGCATATATGAACTCTA 309
Db      2305 GCTTATTTCAAGGGCGTTATCTACGCCCTACAGGTGAGAGAAATGATACGAAACG 2364
Qy      310 TTTCCAACTTATCTGCAAAAATAGATAGTCTAAATTTAAACCATATACAGTTAT 369
Db      2365 TATCCAAAGTATCTGATCAAAAAGTAGAGAGAGTGTATTAACCATACAGAAATAT 2424
Qy      370 CGAGTAAGAGGGTTTGGGAGTAGTAAGATTTGAATTTAATGTTAACGCTTACGGG 429
Db      2425 AGATTTGAGAGGGTTTGTGCGAAGCAGTCAAGATTTGAAATTTTCAAAATTCGCA---- 2480
Qy      430 AAAGAAATGATGCTATCATGAAATGTTCCAAATGATTTGGCTTATGACGCCATTCCT 489
Db      2481 -----TCAAGAAACCGAATTTGTAATAATATGATACCGGATGATTTGCTGCGAGATGA 2532
Qy      490 TCATGAGAGATTTACCTGTGATCATCTGCTCATGATGATGACCAAGGATATCTACA 549
Db      2533 TCTCTGTTAATCTGAGATGATG-----A 2557
Qy      550 CCAACAGATGATATGCTCCGATATGATGATGATGATGATGATGATGATGATGATGAT 609
Db      2558 TCAATCGATGACGCAACAAAGATATGATGATGATGATGATGATGATGATGATGATGAT 2617
Qy      610 GTGAAGTGTACGATCGTCAATTCATTTGATTTGATATTTGACACCGGAGAAATGATACA 669
Db      2618 GTGAAGG-----CATGAGTCTCTATTTCTATTTGATGATGATGATGATGATGATGAT 2667
Qy      670 AATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
Db      2668 AATGAAATGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2727
Qy      730 GTAGGAAATCTTGAAGTATGAAAGAACCACTTAAACAGTGAAGCATTTGGCATGTG 789
Db      2728 CTCGGAACCTTGAAGATTTGTCGAAGAGGACCTTTATCAGAGACGATTTAGAACGCTTG 2787
Qy      790 AAACAAAGAAAGAAATGGAACCAACATGAGAAAGAAACCTTGGGAAACCAACAA 849
Db      2788 CAAAGAGAAACAACGATGAAATTCMAATGCAAGAGACGTAAGAAACGATAGA 2847
Qy      850 GCCTATGATCCAGCAAAACAGCTGTGATGATGATTTTCAATGAAACAGAGTTACAC 909
Db      2848 AGTATATGCGATCCAAACAAACGGGTAGATCGTTATATATGCGGATATCAGATCAGACA 2907
Qy      910 TATCATATTACTTTAGA-----TCATATTCAAAACGTCATCGACTGTCAGTCGATT 963
Db      2908 CTGAATCCGTGATGTAGATTTACAGATCTTACTGGGCCCCAAGATCTGATACAGTCATT 2967
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QY 1264 GAAAAAGGATGTAACAGATGATGATTGTAATGGAACAGAAACCTTAAGTTCACT 1323
DB 3986 GAAATGATATGTAAGTATCCGTGATGTGGAAATCAAAACAGAAACGCTTCTTTAGT 4045
QY 1324 TCTTGGCAAGAG 1336
DB 4046 GCAGCGATTATG 4058

RESULT 11
US-11-108-389-17
; Sequence 17, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pepticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17

Query Match 17.9%; Score 302.6; DB 11; Length 4874;
Best Local Similarity 55.4%; Pred. No. 3.9e-58;
Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;

QY 22 AGTACGAAAAATACGTTAAATAAGAAACAGACAGATTATGAATGATCAAGCGGCATT 81
DB 2783 AATACAAAGATGCGCTTACGACCAAGCGCTAACGATTATGAAGTGCAATCAAGCGCAAC 2842
QY 82 TCTATAGATGTATGTACAGATGACAAATCTCTCAGAAAAATATATGTTATGGATGAA 141
DB 2843 TTAAGGAAATGCGCTATCGATGATTTGTATCCAAATGAAAAAGATGTTATTTATGATGA 2902
QY 142 ATAAAACTGGCAAAACAACTTATGTCAGTCTCGTATCTACTCCAAATGGAAGCTT---- 197
DB 2903 GTGAGGAGGCAAAACGCTCAGTGAGGACGTAATTTGCTTCMAAGATCAAGATTTCCAA 2962
QY 198 -----TTCTGGAAATGATGACATTCGGTATGATATTATCATAGATCCAAATAT 249
DB 2963 GAGATTAATGAGAAATGCGTGCAGCAAGTACGGGAATGAGTTATGAAGGGGAT 3022
QY 250 CCTATTTTAAAGAAAAATTTCTACAGATGCGTGAGACAAGACATATATGAACTCTTA 309
DB 3023 GCTTATTCAGAGGGCGTTATCTACGCTACCAAGGTGAGAGAAATATAGATACGAAACG 3082
QY 310 TTTCCAACTATATCTGTCAAAAAATAGATGAGTCTTAATTTAAACCATATACAGTTAT 369

DB 3083 TATCCAGATATCTGTATCAAAAAAGTAGAGGAAGGTATTTAAACCATACAAAGATAT 3142
QY 370 CGAGTAAAGGGGTTTGTGGGAAAGTAGTAAGATTTGAATTTAAATGATTAACGCTTACGGG 429
DB 3143 AGATGAGAGGGTTTGTGGAAGCAGTCAAGATTTGAAAAATTTTCACAATTCGTCA---- 3198
QY 430 AAAGAAATTTGATGCTATCATGATGATTTCCAAATGATTTGGCGCTATATGACGCTTAATCCT 489
DB 3199 -----TCAAGCGAACCGAATGTGTAATAAATGATACCGGATGATTTGTCGACAGATGA 3250
QY 490 TCATGTGAGATTTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAAGGATATCTTCA 549
DB 3251 TCTCCTGTTAACTCGGATGCTAGT-----A 3275
QY 550 CCAACAGATGATATGCTCCGATATGTATGATGATCCCGCAAAATATATGATGAAGAT 609
DB 3276 TCAATCGATGACAGCAACAAAGATGTGAATAGCCGTTTGAAGTAAAGAACCGTTCTG 3335
QY 610 GTGAAGTTCACGATCCGATCCATTTGATTTTCAATTTGACACCGGAGAAATGATATCA 669
DB 3336 GTGAAGCG-----CATGAGTTCCTATTTCTATTTGATACAGGTAAATGATATAC 3385
QY 670 AATACAAATGTAGTATGATGATGTCTTATTAATAATTTCTAATCCAGATGATATGCTTACA 729
DB 3386 AATGAAATTCAGGAATATGCGTTGATTTTAAGATTTACGACCCAGAGGATATGCAACA 3445
QY 730 GTAGGAAATCTAAGATGATTTGAAGAGAACCACTAACAGTGAACATTTGGACATGTG 789
DB 3446 CTCGGAACCTTAGAATGTGTCGAGAGGACCTTTATCAGAGACGCAATTGAACGCTTG 3505
QY 790 AAACAAAGGAAAAAGAAATGGAACACACATGAGAAAGAAAAAGTTGGAAAAACAACA 849
DB 3506 CAAGAGAGAACCAACAGTGAAGATTTAAATGACAAAGACGTAAGAAACATATGA 3565
QY 850 GCCTATGATTCAGCAAAACAGCTGTAGATGATATTTAACAATGAACAAGATTAC 909
DB 3566 AGGTATATGCGATCGAAACAAAGCGGTATGCTTTATATGCGATTTACAGATACGAA 3625
QY 910 TATCATATTAATCTTGA-----TCATATCAAAACGCTGATGCACTGATACATGAT 963
DB 3626 CTGAATCCTGATGTGATGATTAACAGATCTTACTGCGGCCAAAGATCTGATACAGTCAAT 3685
QY 964 CCTATGATATCAATATTTGTTTACCGAATGCTCCAGATTTGAATATGATATATCA 1023
DB 3686 CCTTACGATATTAAGAAATGTTCCAGAAATATCCAGGATGAACTATACGAAGTTTACA 3745
QY 1024 GAGTTAAACGACGATCATGCAAGGTTATTAATTTATGATGACAGAAATGCTATACA 1083
DB 3746 GAATTAACAGATCGACTCCACAAAGCGTGAAGTTGTATGATCAGCGAAATGCCATACA 3805
QY 1144 CAATGATGAGCTTCAAGTATTAATTTATTAATTTGAAGCGGGGTATCTCAAAAC 1203
DB 3866 CAATCAATTCATACATCTGTCTGTGATTTCCAACTGGATGACAAATTTGCGAACG 3925
QY 1204 TTGCATGCTCAAGATCATGATGATGATGTTAGCTGATGATGCGCAAAAAAGAGAACT 1263
DB 3926 TTTACAGTTCAACGAAATCAAAAGATATGTGTTTACAGATTTCTGCAAGAAAGAGGGA 3985
QY 1264 GAAAAAGGATATGTAACAGATGATGATTTGAATGGAAGACAGAAACCTTAAGTTCACT 1323
DB 3986 GGAATGATATGTAAGTATCCGTGATGTGGAATCAAAACGAAACCTTACTTTTAGT 4045
QY 1324 TCTTGGCAAGAG 1336
DB 4046 GCAGCGATTATG 4058

RESULT 12
US-11-224-624-17

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; Sequence 17, Application US/11224624
; GENERAL INFORMATION:
; Publication No. US20060021096A1
; APPLICANT: Abad, Andre
; APPLICANT: Dong, Hua
; APPLICANT: Hermgum, Rafael
; APPLICANT: Lu, Albert
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Rice, Janet
; APPLICANT: Schneper, Eric
; APPLICANT: Wong, James
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/297402
; CURRENT APPLICATION NUMBER: US/11/224,624
; PRIOR FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/746,914
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)_(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-11-224-624-17

Query Match      17.9%; Score 302.6; DB 11; Length 4874;
Best Local Similarity 55.4%; Pred. No. 3.9e-58;
Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;

QY 22 AGTACGAAATATACGTTAAATAAGAAACGACAGATTATGAAATGATCAACGGCCATT 81
DB 2783 AATACAAAGATGCTTACGACACGACGCGTAACGATTAATGAATCAAGCGCAAC 2842
QY 82 TCTATAGATGATCTCATGATGAAACAAATCTCTCGAAGAAATATATGTTATGGATGA 141
DB 2843 TTAGTGATGATCTATCGATGATTTGTAATCAAAATGAAACGATGTTATTTGATCA 2902
QY 142 ATAAAGCTGCAAAACCTTAGTCACTCTGTAATCTACTCAAAATGAGACTT---- 197
DB 2903 GTGAGAGAGCGAAACGCTCGATGAGGACGTAATTTGCTTCAAGATCCGATTTCCA 2962
QY 198 -----TTCTGGAAATGATTTGACATTCGGTAATGATTAATCATAGATCCAAATAT 249
DB 2963 GAGATTAATGAGAAATATGCTGACGCGCAAGTACGGAAATGAGATTAAGAGGGAT 3022
QY 250 CCTATTTTAAAGAAATTTCTACAGATGCTGAGACGACAGATATATGAACTCTA 309
DB 3023 GCTTATTCAAAGGCGTTATCTACCTTACCGAGGTGAGAGAAATGATACGGAACG 3082
QY 310 TTTCACCTATATCTGTCAAAATAATAGATAGTCTAATTAATTAACCATATACGTTAT 369
DB 3083 TATCCAACTATCTGTATCAAAATAGAGAGAGTGTATTAACCATACAGATATAT 3142
QY 370 CGAGTAAGAGGTTTGTGGAAAGTAGTAAGATTTGAAATTATAGTAACAGTTACGGG 429
DB 3143 AGATGAGAGGTTTGTGGAAAGTAGTAAGATTTGAAATTATAGTAACAGTTACGGG 3188
QY 430 AAAGAAATGATGCTATCATGATTTTCCAAATGATTTGGCTATATGACGCTTAATCT 489
DB 3199 -----TCAAGCAACCGAATTTGTAATAAATGATACCGAGTATTTCTCGCAATGTA 3250
QY 490 TCATGTGAGATTTATCGCTGTGAATCATGCTTCAGTATGTAGGCAAGGATCTCTACA 549

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DB 3251 TCTCTGTTAACCTGGATGGTAGT-----A 3275
QY 550 CCAACAGATGATATGCTCCCGATATGATGATGATGATGATGATGATGATGATGATGAT 609
DB 3276 TCAATGATGACGAGCAAAAGATATGATGATGATGATGATGATGATGATGATGATGAT 3335
QY 610 GTGAAGTGTACGATTCGATTCATTTGATTTTGTATTTTGTATTTTGTATTTTGTATTTTGT 669
DB 3336 GTGAAGG-----CATGAGTTCTATTTCTTATTTATGATGATGATGATGATGATGAT 3385
QY 670 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
DB 3386 AATGAAATGACGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3445
QY 730 GTAGGAATCTGAAGATCTTGAAGAGACCTTAACAGTGAAGATGATGATGATGATGATG 789
DB 3446 CTCGGAACCTGAGATTTGTCGAGAGGACCTTTATCAGAGAGCGATTAAGAACGCTTG 3505
QY 790 AAACAAAGGAAAGAAATGGAACCAACATGGAAGAAAGAAAGGTTGGAAACACACAA 849
DB 3506 CAAGAGAGAGAACACAGTGAAGATTCAAATGACAGAGAGCGTGAAGAAACAGATGA 3565
QY 850 GCTATGATCCAGCAAAACAGGCTGTAGATGATGATGATGATGATGATGATGATGATGAT 909
DB 3566 AGGTATATGCGATGAGAAACAGCGGTAGATGATGATGATGATGATGATGATGATGATGAT 3625
QY 910 TATCATTTACTTTGA-----TCATATTCAAACGCTGATGATGATGATGATGATGAT 963
DB 3626 CTGAATCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3685
QY 964 CCTATGATATCATTAATTTGTTACCGAATGCTCAGATGATGATGATGATGATGATGATGAT 1023
DB 3686 CTTATGATATTAACGAAATGTTCCAGAAATACAGAGATGATGATGATGATGATGATGAT 3745
QY 1024 GAGTTAAACGACGATATCATGACAGGTTATTAATTAATGATGATGATGATGATGATGAT 1083
DB 3746 GAATTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3805
QY 1084 AATGATGATTTACAGAGATTAACAGAGATGATGATGATGATGATGATGATGATGATGAT 1143
DB 3806 AATGATGATTTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3865
QY 1144 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
DB 3866 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3925
QY 1204 TTGATGCTCAAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
DB 3926 TTACAGTTCAACGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3985
QY 1264 GGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
DB 3986 GGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4045
QY 1324 TCTTGGAGAGAG 1336
DB 4046 GCAAGCATTTATG 4058

RESULT 13
US-11-058-727-18
; Sequence 18, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F. H. Wong

```

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; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6613
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0) ... (0)
; OTHER INFORMATION: Genomic Cry121b-2
US-11-058-727-18

Query Match      17.9%; Score 302.6; DB 11; Length 6613;
Best Local Similarity 55.4%; Pred. No. 4.1e-58;
Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;

QY 22 AGTACAAAATACGTTAAATAGAAAGACAGATTATGAAATAGATCAAGCGGCATT 81
DB 3318 AATACAAAAGATGCTTACGACACGCGCTACGATTAATGAAATCAAGCGGAAAC 3377
QY 82 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
DB 3378 TTAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3437
QY 142 ATAAAGTGGCAAAACAACTTACGATGATGATGATGATGATGATGATGATGATGAT 197
DB 3438 GTGAGAGAGCAAAAGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 3497
QY 198 -----TTCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
DB 3498 GAGATTAATGAGAAATGCGTGCAGCGCAATGCGGAATGAGTTATGAGAGGGAT 3557
QY 250 CCTATTTTAAAGAAATTTCTACAGATGCGTGCAGCGCAATGCGGAATGAGTTAT 309
DB 3558 GCTTATTCAGAAAGGCGTATATCTACGCTACCGAGTGCAGAGAAATGATACGAAACG 3617
QY 310 TTTCCAACTATATCTGTCATAAAATAGATGATGATGATGATGATGATGATGATGAT 369
DB 3618 TATCCAACTATATCTGTCATAAAATAGATGATGATGATGATGATGATGATGATGAT 3677
QY 370 CGAGTAAAGAGGTTTGTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 429
DB 3678 AGATTAAGAGGTTTGTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 3733
QY 430 AAAGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489
DB 3734 -----TCAAGCAAGCAAGATGTAAGAAATGTAAGCAAGATGATGATGATGAT 3785
QY 490 TCATGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
DB 3786 TCTCCGTAACTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3810
QY 550 CCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
DB 3811 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3870
QY 610 GTGAAGTGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
DB 3871 GTGAAGCG-----CATGAGTTCTGATATCTGATGATGATGATGATGATGATGAT 3920
QY 670 AATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
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DB 3921 AATGAAATGCAAGATATGCGTTGATTTAAGTTAAGTACGACCCGAGGATATGCAACA 3980
QY 730 GTAGGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789
DB 3981 CTCGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4040
QY 790 AAACAAAGGAAAGAAATGGAACAACAATGAGGAAAGAAAGAAAGAAAGAAAGAAAG 849
DB 4041 CAAAGAAAGAAACAACGAGGAAAGATTCAAATGACAAAGAAAGCGTGAAGAAACAGATGAC 4100
QY 850 GCTATGATCCAGCAAAACAGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 909
DB 4101 AGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4160
QY 910 TATCATATTTACTTTAGA-----TCATATTCAAAACGCTGATGATGATGATGATGATGAT 963
DB 4161 CTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4220
QY 964 CCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023
DB 4221 CCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4280
QY 1024 GAGTTAAACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
DB 4281 GATTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4340
QY 1084 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
DB 4341 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4400
QY 1144 CAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
DB 4401 CAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 4460
QY 1204 TTGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
DB 4461 TTTACAGTTCAACCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4520
QY 1264 GGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
DB 4521 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4580
QY 1324 TCTTGCAGAAAG 1336
DB 4581 GCAAGGATGATG 4593

RESULT 14
US-11-108-389-18
; Sequence 18, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
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NUMBER OF SEQ ID NOS: 134
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 18
 LENGTH: 6613
 TYPE: DNA
 ORGANISM: Bacillus thuringiensis
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0)..(0)
 OTHER INFORMATION: Genomic Cry12Ib-2
 US-11-108-389-18

Query Match 17.9%; Score 302.6; DB 11; Length 6613;
 Best Local Similarity 55.4%; Pred. No. 4,1e-58;
 Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;

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QY 22 AGTACGAAATAATACGTTAAATAATAGAAACGACAGATTATGAAATAGATCAACGGCCATT 81
DB 3318 AATACAAAAGATGGCTTACGACGAGCGTACGATTTATGAAATGAAATCAACGGCCAAAC 3377
QY 82 TCTATGAAATGATGTCAGATGAAACAAATCTCTAGAGAAAATAATATGATGATGAA 141
DB 3378 TTAGTGAATGCTTATCGGATATTTGATCCAAATGAAAAAGATTTGATTTGATGCA 3437
QY 142 ATAAAGCTGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAATGGAAGCTT---- 197
DB 3438 GTGAGAGAGCAAAACGCTTCACTGAGCAGCTAATTTGCTTCAGATCCAGATTTCCAA 3497
QY 198 -----TTCTGGAAATGATGACATTGCGTAATGATATTATCATAGATCAATAT 249
DB 3498 GAGATTAATGAGAAAATGCTGACGCGCAATGACGGAAATTGAGTTATGAAAGGGAT 3557
QY 250 CCTATTTTAAAGAAAATTTCTACAGATGCGTGAAGCAGACGACATATAGAACTCA 309
DB 3558 GCTTATTTCAAGGGCGTTATCTACGCCCTACAGGTCGAGGAATATGATTCGAAAACG 3617
QY 310 TTTCCAACTTATCTGTCAAAAAATAGATGAGTCTAAATTTAAACCATATACAGTTAT 369
DB 3618 TATCCAAAGTATCTGTATCAAAAAGTAGAGAGAGTATTTAAACCATATACAGATAT 3677
QY 370 CGAGTAAGAGGTTTGTGGAGTAGTAAGATTTGAAATTATAGGTAAACAGTTACGGG 429
DB 3678 AGATTGAGAGGGTTTGTGGAGTAGTCAAGGATTTGAAATTTTCACAATTGCTCA---- 3733
QY 430 AAAGAAATTTGATGATCATGATGATCCAAATGATTTGGCTATATGAGGCTATCT 489
DB 3734 -----TCAACGAAACGGAATTTGAAAAATGACCGAGTATTTGTCAGATGTA 3785
QY 490 TCATGTGAGATTTATCGCTGTGAATCATGCTCAGTATGTGAGCAAGGATCTCTACA 549
DB 3786 TCTCTGTTAACTCGGATGCTAGT-----A 3810
QY 550 CCAACAGATGATATGCTCCGATATGATGATGATGATGATGATGATGATGATGATGAT 609
DB 3811 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3870
QY 610 GTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
DB 3871 GTGAGGCG-----CATGATTTCTTATCTTATGATGATGATGATGATGATGATGATGAT 3920
QY 670 AATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
DB 3921 AATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3980
QY 730 GTAGGAAATCTTGAAGTCAATGAAGAGACCTTACAGGATGATGATGATGATGATGATGAT 789
DB 3981 CTCGGAACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4040
QY 790 AAACAAAGGAAAGAAATGAAACACATGAGGAAAGAAAGGTTGGGAAACACACACA 849
DB 4041 CAAGAGAAAGAAACACATGAGGAAAGTTCAAATGACAGAAAGCGTGAAGAAACACATGAG 4100
QY 850 GCTTATGATCCAGCAAAACAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 909

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DB 4101 AGGTATATGATGATGAAACAGCGGTAGATGTTTATATGCGATTTATCAGATCAGCAA 4160
QY 910 TATCATTTACTTTTGA-----TCAATTTCAAAACGCTGATCCAGTGTACAGTCAATT 963
DB 4161 CTGAATCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4220
QY 964 CCGTATGATATCAATTAATGTTTCCGAATGCTCAGGTATGAACTATGATGATGATGATGATGAT 1023
DB 4221 CTTTACGATATTAACGAATATTTCCAGAAATACAGGATGAACTATGATGATGATGATGATGAT 4280
QY 1024 GAGTTAAACGACGATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
DB 4281 GAATTAACAGATTCAGCTCCAAACAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 4340
QY 1084 AATGTGATTTTACCAAGATTTACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
DB 4341 AATGTGATTTTTCGAAAGGTTAAGTAAATGGAATGCAACGCTGCGGTGAAATGATCA 4400
QY 1144 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
DB 4401 CAATCAATCATATCTTCTTGTGATTTCCAACTGAGTGAAGCAAGTTTCCGACAG 4460
QY 1204 TTGATGCTCAAGATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
DB 4461 TTTACAGTTCAACGAATCAAAAGATATGTTTGAAGTTACTGCGAAGAAAGAGGGTGA 4520
QY 1264 GAAAGAGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
DB 4521 GAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4580
QY 1324 TCTTGGCAAGAG 1336
DB 4581 GCAAGCATTTATG 4593

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RESULT 15
 US-11-224-624-18
 Sequence 18, Application US/11224624
 Publication No. US20060021096A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Andre
 APPLICANT: Dong, Hua
 APPLICANT: Herrmann, Rafael
 APPLICANT: Lu, Albert
 APPLICANT: McClutchen, Billy F.
 APPLICANT: Rice, Janet
 APPLICANT: Schepers, Eric
 APPLICANT: Wong, James
 TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
 TITLE OF INVENTION: Activity
 FILE REFERENCE: 35718/297402
 CURRENT APPLICATION NUMBER: US/11/224,624
 CURRENT FILING DATE: 2005-09-12
 PRIOR APPLICATION NUMBER: 60/391,786
 PRIOR FILING DATE: 2002-06-26
 PRIOR APPLICATION NUMBER: 60/460,787
 PRIOR FILING DATE: 2003-04-04
 PRIOR APPLICATION NUMBER: 10/606,320
 PRIOR FILING DATE: 2003-06-25
 PRIOR APPLICATION NUMBER: 10/746,914
 PRIOR FILING DATE: 2003-12-24
 NUMBER OF SEQ ID NOS: 143
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 18
 LENGTH: 6613
 TYPE: DNA
 ORGANISM: Bacillus thuringiensis
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0)..(0)
 OTHER INFORMATION: Genomic Cry12Ib-2
 US-11-224-624-18

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GenCore version 5.1.7
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(without alignments)
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Title: US-10-781-979-6

Perfect score: 1686
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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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- 8: /cgn2_6/ptodata/1/ina/BACKFILES1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	763.8	45.3	3543	6	PCT-US94-07902-27
3	379	22.5	3504	3	US-10-089-678-2
4	379	22.5	3690	3	US-10-089-678-3
5	357.4	21.2	3797	2	US-07-915-203-1
6	357.4	21.2	3797	2	US-08-272-887-1
7	357.4	21.2	3797	2	US-08-789-449-1
8	311.8	18.5	3471	2	US-07-876-280-29
9	311.8	18.5	3471	2	US-07-812-180A-1
10	311.8	18.5	3471	2	US-08-315-468-1
11	311.8	18.5	3471	3	US-07-941-650A-1
12	303	18.0	3414	2	US-07-973-320-3
13	299.8	17.8	3414	2	US-07-973-320-1
14	286.6	17.0	3507	2	US-08-315-468-3
15	271.4	16.1	3759	2	US-08-542-921-1
16	271.4	16.1	3759	2	US-08-880-685-1
17	271.4	16.1	3759	2	US-08-880-684-1
18	269.6	16.0	3453	3	US-09-002-285-75
19	269.6	16.0	3453	3	US-09-589-477-75
20	269.6	16.0	3453	3	US-10-099-285A-75
21	269	16.0	3522	2	US-08-040-751-4
22	269	16.0	3522	2	US-08-291-368-1
23	269	16.0	3522	2	US-08-962-190-1
24	269	16.0	3522	6	PCT-US95-10310-1

25	269	16.0	3522	9	5164180-3	Patent No. 5164180
26	269	16.0	4344	2	US-08-532-547-4	Sequence 4, Appli
27	269	16.0	4344	2	US-08-378-656B-4	Sequence 4, Appli
28	269	16.0	4344	3	US-08-455-838-4	Sequence 4, Appli
29	269	16.0	4344	3	US-09-019-809-4	Sequence 4, Appli
30	269	16.0	4344	3	US-09-471-177-4	Sequence 4, Appli
31	269	16.0	4344	3	US-09-220-806-4	Sequence 4, Appli
32	268.8	15.9	3471	3	US-09-002-285-73	Sequence 73, Appli
33	268.8	15.9	3471	3	US-09-589-477-73	Sequence 73, Appli
34	268.8	15.9	3471	3	US-09-661-322A-27	Sequence 27, Appli
35	268.8	15.9	3471	3	US-10-099-285A-73	Sequence 73, Appli
36	265.8	15.8	3504	3	US-09-661-322A-39	Sequence 39, Appli
37	265.8	15.8	3504	2	US-08-291-368-3	Sequence 3, Appli
38	261.2	15.5	3504	2	US-08-962-190-3	Sequence 3, Appli
39	261.2	15.5	3504	6	PCT-US95-10310-3	Sequence 3, Appli
40	261	15.5	3531	3	US-08-855-160-3	Sequence 3, Appli
41	261	15.5	3531	3	US-08-855-160-5	Sequence 5, Appli
42	261	15.5	3531	3	US-08-855-160-7	Sequence 7, Appli
43	260.6	15.5	3713	2	US-08-100-709-1	Sequence 1, Appli
44	260.6	15.5	3713	2	US-08-176-865-1	Sequence 1, Appli
45	260.6	15.5	3713	2	US-08-474-038-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-224-024-27
; Sequence 27, Application US/09224024
; Patent No. 6056953
; GENERAL INFORMATION:
; APPLICANT: Leslie Hickie
; APPLICANT: Jewel Payne
; TITLE OF INVENTION: Materials and Methods for the Control of
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3543 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-224-024-27
Query Match 45 %; Score 763.8; DB 3; Length 3543;
Best Local Similarity 71.9%; Pred. No. 1.3e-183;

Matches 1050; Conservative 0; Mismatches 387; Indels 24; Gaps 3;

QY 2 TGAGTCTATGTTTCAAGTAGTACGAAAAATGCTTAAAAATGAAACGACAGATTATG 61
Db 2090 TTAATATATTTTATGCAAAATCCTATAAAAACATCTTACATCGAACTTACAGATTATG 2149
QY 62 AAATAGATCAAGCGGCGCATTTCTATAGAAATGATGTCAGATGAACAAATCTCGGAAA 121
Db 2150 ACATAGATCAAGCGGCGCAATCTTGTGGAATGATTTCTGAAAGAAATTAATCCAAAGAAA 2209
QY 122 AAATATGTTATGGGATGAAATAAACTGGCAAAACAATTAGTCAGTCTGTAATCTAC 181
Db 2210 AAATGCTGTTATTTAGATGAAGTAAATGCGAAACAATTAGTCAATCTGAAATGTAC 2269
QY 182 TCCAAAATGAGACTTT-----TCTGGGAATGATGGACATTCCGTAATGATATTATCA 235
Db 2270 TTTCAAAACGGGGATTTTGAAATCGGCTACGCTGTGGTGGACAAACAGTATATATACAA 2329
QY 236 TAGGATCCAATATCTTATTTTAAAGAAATTTCTACAGATGCGTGAGACAGAGACA 295
Db 2330 TTCAAGAAAGATGATCTTATTTTAAAGGCGATTACCTTCAATATGCTGGGCGAGAGAAA 2389
QY 296 TATATGGAATCTTATTTTCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTTAAAC 355
Db 2390 TTGATGATGATATTTTCCGACTATATATCCAAAAATTTGATGAATCAAAATTTAAAC 2449
QY 356 CATATACAGTTATCGAGTAAGAGGTTTGTGGGAAGTAGTAAGATTGAATTTAATGG 415
Db 2450 CGTATACACGTTACTGATTAAGGGATTTGTAGGAAGTAGTAAGATCTAAGACTAGTGG 2509
QY 416 TAAACGTTACGGGAAAGAAATTTGATGCTATCATGAATGTTCCAATATTGGCCTATA 475
Db 2510 TTTTACCGTATGGGAAAGAAATTTGATGCTATCATGAATGTTCCAGCTATTTAAACTATC 2569
QY 476 TGCAGCCTAATCTTCAATGTAAGATTATCGCTGTAATCATCGTCTGAGTAGTGACC 535
Db 2570 TGTATCTTCTTAC-----CTTGATGTGAAAGGGCTAATGCTTGTGAGAGCT 2617
QY 536 AAGGATCTTACACCAACAGATGATATGCTCCGATATGTATGATGCCCCGAAATA 595
Db 2618 CCGCTGTGCGGCTTAACTTTGGGAACACTTCTGATATGCTAATTCATGCAATATGATA 2677
QY 596 TAGATAGAAAGCATGTGAAGTGTCAAGATCGTCAATCTTGAATTTTCAATTTGACACG 655
Db 2678 CAGGAAAAACATGTCTATGTCAAGATTTCCCATCAATTTAGTTTCACTATGATACAG 2737
QY 656 GAGAAGTAGATACAATAACAATGTAGTATGATGTTCTTATTAATAATTTCTAATCCAG 715
Db 2738 GGGCATTAGATACAATAATAATATAGGGGTTGGGTCATGTTTAAATATCTTCTCCAG 2797
QY 716 ATGATACGCTACAGTAGGGAATCTAAGATCTTGAAGAAAGACCACTAACAGTGAAG 775
Db 2798 ATGATATCGCATCTTATGATATTTAGAAATTTGAAGAAAGGCGCAATATAGGGGAAG 2857
QY 776 CATGGGACATGTGAAACAAAGAAAGAAATGGAACCAACATGGAAGAAAAAGCTT 835
Db 2858 CACTGTCAAGCGGTGAACACATGGAAGAAATGGAACGATCAAAATGGAACAAAAAGCTT 2917
QY 836 GGGAAACAAACAAAGCTTATGATCCAGAAAAAGGCTGTAGATGATATTTTCAAAATG 895
Db 2918 CGGAAACAAACAAAGCATATGATGAGGAAACAAAGCATTAATGCTTATTTCAAAATG 2977
QY 896 AACAGA-----GTACACTATCATATTACTTTAGATCATATTTCAAAACGCTGATGAC 949
Db 2978 TACAAAGATGAGGCTTTACAGTTTGATGACACATCGCTCAAAATTCAGTACCTGATTT 3037
QY 950 TGTATACAGTGCATTCCTATGTATACCAATATTTGGTTACCAAGTCTCAGATATGAAT 1009
Db 3038 TGTATACATGATTCATATGTATGTAATGATGTTGTTGTCAAGATGTTCCAGATATGAAT 3097
QY 1010 ATGATGTATATCAAGAGTTAAACGACGATATCATGCAAGGTTATATTTATATGATGAC 1069
Db 3098 ATGATATCTATGTAGAGTTGATGACAGAGTGGACAGAGCGCTTATTTGTATGATACAA 3157

QY 1070 GAAATGCTATPACAAATATGATGACTTTACAGAGATTACAGGATGCGACACAGAAA 1129
Db 3158 GAAATATATTTAAAAATGGTATTTTACACAGGGGTAATGGGGTGCATGTAACTGAAA 3217
QY 1130 ATCCGCGGTACACAAATGATGATGAGACTTCAGTATTAGTTCTATCAAAATTTGAGCGCG 1189
Db 3218 ATGCAAGCTACAAACAAATGATGATGTTTCTGTATTTGTTCTATATTTTGGATGCTG 3277
QY 1190 GGGTATCTCAAACTTGATGCTCAAGATCATCATGATATGTTTACGTTGATTTGCCA 1249
Db 3278 GCGTATCTCAAAATGTCCATCTCCAACTATCATGAGTATGTTTACGTTTATTTCCCA 3337
QY 1250 AAAAAGAGACCTGGAAAAAGGATTTAAGATGATGATTTGAAATGAAAGAGAGAAA 1309
Db 3338 AAAAAGAGACCTGGAAAAAGGATTTAAGATGATGATTTGAAATGAAAGAGAGAAA 3397
QY 1310 CACTTAAGTTCATCTTCTGGCAAGAAAGATATATGACAAAAACAGTAGAGTATTTCCAG 1369
Db 3398 AATTGACGTTTACGTTCTTGTGAAGAAAGATATATTAAGAAACAGTAGATGATTTCCAG 3457
QY 1370 AAAGTATCGGTACGATTTGAATTAAGAAACCGAAGGTACATTTATATAGATACGA 1429
Db 3458 ATACAGATCGGTACGATTTGAATTAAGAAACCGAAGGTACATTTATATAGATACGA 3517
QY 1430 TCGAGTTGCTTGTATGCAAG 1450
Db 3518 TTGAATTAATTTGCATGAACG 3538

RESULT 2
PCT-US94-07902-27
Sequence 27, Application PC/TUS9407902
GENERAL INFORMATION:
APPLICANT: Street address: 4980 Carroll Canyon Road
APPLICANT: City: San Diego
APPLICANT: State/Province: California
APPLICANT: Country: US
APPLICANT: Postal code/Zip: 92121
APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991
APPLICANT: Telex number:
TITLE OF INVENTION: Materials and Methods for the Control of
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3543 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07902-27

Query Match 45.3%; Score 763.8; DB 6; Length 3543;

Best Local Similarity 71.9%; Pred. No. 13e-183; Indels 24; Gaps 3;

Matches 1050; Conservative 0; Mismatches 387; Indels 24; Gaps 3;

2 TGAGTCCTATGTTTACAGTAGTACGAAAAATACGTTAAATAATAGAAAAGACAGATTATG 61
Db TTAATACATTTTATCCAAATCCTATATAAAAAACATTTTCAATCAGAACCTTACAGATTATG 2149
Qy 2090 TTAATACATTTTATCCAAATCCTATATAAAAAACATTTTCAATCAGAACCTTACAGATTATG 2149
Db 62 AAATGATCAAGCGGCCATTTCTATAGATGATGTCAGATGACAAATAATCTCAGGAAA 121
Qy 2150 ACATGATCAAGCGGCCAATCTTGGAATGATTTTCGAAAGAAATTAATCCAAAGAAA 2209
Db 122 AAATGATGTTTATGGAGTAAATAAACGCGAAACAACTTATGATGTCGTAATCTAC 181
Qy 2210 AAATGCTTTTATGATGATGATTAATAATGCGAAACAACTTATGATGTCGTAATCTAC 2269
Db 182 TCCAAATGAGACTTT-----TCTGGAAATGATGGAATTCGTAATGATATTATCA 235
Qy 2270 TTTCAAAAGGGGATTTTGAATGGCTAGCTGTTGGAACAACAGTGAATATATACAA 2329
Db 236 TAGGATCCATATATCTTATTTTAAAGAAAATTTCTACAGATGCTGAGACAGACACA 295
Qy 2330 TTCAAGAAAGATGATCTTATTTTAAAGGCAATTACCTTATGATGCTGAGGCGAAGAAA 2389
Db 286 TATATGAACTCTATTTCCAACTATCTGTCGAAAAATGATAGTCTAATTTAAAC 355
Qy 2390 TTGATGATCAATATTTCCGACCTATATATTCGAAAAATGATGATTAATTTAAAC 2449
Db 356 CATATACAGTATTCGATGATGAGGGTTTGCGGAAGTATGAAAGATTGAAATTAATG 415
Qy 2450 CGTATACAGTATTCGATGATGAGGGTTTGCGGAAGTATGAAAGATTGAAATTAATG 2509
Db 416 TAAACGTTACGGGAAAGAAATTTGCTATCATGATGTTCCAAATGATTTGGCCATA 475
Qy 2510 TTTTCAGCTATGCGGAGAAATTTGATGCTATCATGATGTTCCAAATGATTTTAACTATC 2569
Db 476 TGCAGCCTATCTTCATGATGAGATTTATCGCTGGAATCATCGTCTCAGTATGAGGC 535
Qy 2570 TGTATCTCTTCTAC-----CTTGATGTTGAAGGGTCTAATCGTTGTGAGAGCT 2617
Db 536 AAGGCTATCTACACCAACAGATGATATGCTCCGATATGATCATGCCGCAAAATA 595
Qy 2618 CCGCTGTGCGGCTTAACATTTGGGAACATTTGATATGCTGATATCATGCCAATATGATA 2677
Db 596 TAGATGAAAGCATGTGAATGTCACGATGCTATCATGATTTTCAATTTTCAACACCG 655
Qy 2678 CAGGGAAGAAAGCATGTGATGTCAGATTTCCATCAATTTAGTTTCACTATGATACAG 2737
Db 656 GAGAGTATGATCAATCAATCAATGATGATGATGCTTATTAATAATTTCTAATCCAG 715
Qy 2738 GGGCAATTAAGATCAATCAATCAATTAATTAATTAATTAATTAATTTCTCAG 2797
Db 716 ATGATATGCTACATAGAGGAATCTAGAAGTATTAAGAAAGACCACTAACAGGTGAAG 775
Qy 2798 ATGATATGCTACATAGAGGAATCTAGAAGTATTAAGAAAGACCACTAACAGGTGAAG 2857
Db 776 CATTGGCAATGTGAACAAAGAAAGAAATGGAACACACATGAGAAAGAAAGCGTT 835
Qy 2858 CACTGTCAAGCGGTGAACACATGAGAAAGAAATGGAACACATGAGAAAGAAAGCGTT 2917
Db 836 GGGAAACACAAACCTATGATCCAGAAACAGGCTGTATATGATGATTTTAAATG 895
Qy 2918 CGGAAACACAAACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2977
Db 896 AACAGAG-----GTTACATATATTAATTAATTAATTAATTAATTAATTAATTAAT 949
Qy 2978 TACAAAGATGAGGCTTACAGTTTGAATGACACACTGCTCAATTAATTAATTAATTAAT 3037
Qy 950 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009

Db 3038 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3097
Qy 1010 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1069
Db 3098 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3157
Qy 1070 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129
Db 3158 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3217
Qy 1130 ATGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189
Db 3218 ATGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3277
Qy 1190 GGGTATCTCAAACTTGCATCTCAGATCATCATGATGATGATGATGATGATGATGAT 1249
Db 3278 GGGTATCTCAAACTTGCATCTCAGATCATCATGATGATGATGATGATGATGATGAT 3337
Qy 1250 AAAAAAGAGACCTGGAAGGGTATGATGATGATGATGATGATGATGATGATGATGAT 1309
Db 3338 AAAAAAGAGACCTGGAAGGGTATGATGATGATGATGATGATGATGATGATGATGAT 3397
Qy 1310 CACTTAAGTCACTTCTGGAAGGATATGATGATGATGATGATGATGATGATGATGATGAT 1369
Db 3398 AATGACGTTTACGTTTGTGAAGAGATATATTAAGAGACGATGATGATGATGATGAT 3457
Qy 1370 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1429
Db 3458 ATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3517
Qy 1430 TCGAGTTCCTTTGATGCAAG 1450
Db 3518 TTGAATTAATTTGATGCAAG 3538

RESULT 3

US-10-089-678-2
Sequence 2, Application US/10089678
Patent No. 6962977

GENERAL INFORMATION:

APPLICANT: ASANO, Shinichihiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A

FILE REFERENCE: Q68821
CURRENT APPLICATION NUMBER: US/10/089, 678
PRIORITY FILING DATE: 2002-04-03

PRIOR APPLICATION NUMBER: JP 2000-236140
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: PCT/JP01/06660

NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1

SEQ ID NO 2
LENGTH: 3504

TYPE: DNA

ORGANISM: Bacillus thuringiensis

FEATURE:

NAME/KEY: exon
LOCATION: (1)..(3501)

OTHER INFORMATION:

US-10-089-678-2

Query Match 22.5%; Score 379; DB 3; Length 3504;

Best Local Similarity 56.7%; Pred. No. 4.4e-86; Indels 87; Gaps 4;

Matches 839; Conservative 0; Mismatches 555; Indels 87; Gaps 4;

Qy 22 AGTACGAAATAACGTTAAATAATAGAAAAGACAGATTATGAAATGATCAAGCGGCATT 81
Db 2062 AGTAAAAAGATGCTTACAGACAGAGTAAACGATATTAAGTAAATCAAGCGGCAAC 2121
Qy 82 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141

Db 2122 TTAGTAGATGCTATCCGATAGATTATACCCAAATGAAAAAGCATTTTATGGGATGCA 2181
Qy 142 ATAAAACGCGAAAAACAATTAGTCAGTCGTGTAATCTACTCCAAAATGAGACGTTTCT 201
Db 2182 GTGAAAGGCGAAACGACTGTTCAGGACGATCTTACTTACAGATACAGGCTTTAAT 2241
Qy 202 GGGAAATGAT-----TGACATTCGGTAATGATATTAATCATAGATCCAAATAT 249
Db 2242 AGGATTAATGAGAAAAAGCATGACCGGGAAGTACGGGAATCGAGGTGCGGAAAGGAAAT 2301
Qy 250 CCTATTTTAAAGAAAAATTTCTACAGATGCGTGAGACACAGACATATATGAACTCTA 309
Db 2302 GTTCTGTTTAAAGATCGTTCCTTCGTTTGAAGAAGCGAGAGATGATACGAAACA 2361
Qy 310 TTTCCAACTATCTCTGCAAAAAATAGATAGCTTAATTTAAACCATATACGTTAT 369
Db 2362 TATCCAAAGTATCTCTATCAACAAATAGATATACATTTTAAACCATATACAGATAT 2421
Qy 370 CGAGTAAGAGGGTTTGTGGGAAGTATTAAGATTTGAATTAATGTTAACGTTACGGG 429
Db 2422 AAACCTAAAGGTTTATAGGAAGTATGCAAGATTTAGAGATTTAAATTAATGTCATCGG 2481
Qy 430 AAAGAAATGATGCTATCATGAAATGTTCCAAATGATTTGGCCTATATGCACTTATCT 489
Db 2482 GCAATCAATCGTCAAAAAATGTAACAGATATATCTTGGCAGATGTACTCCCTGTCAT 2541
Qy 490 TCATGTGAGATTAATCGCTGTAATCATGCTCTCAGTATGTAAGCGCAAGGGATTCCTCA 549
Db 2542 TCTTGTGTGGGATCGATCGCTGCAAGTACGACACAGTATG----- 2582
Qy 550 CCAACAGATGATATGCTCCCGATATGTAATGATATGATCCCGCAAAATATAGATGAAGCAT 609
Db 2583 -----AGACGCGAATTTAGACACTCGAAAACAAATGAGAAAAATGGA 2622
Qy 610 GTGAGTGTCAAGTCGTATCATCTATTGATTTTCAATTTGACACCGGGAAGTATGATCA 669
Db 2623 AATATGCTTCTGATTCCTCATGATCTTCTTCCATTTGATGATACAGGGAATATGATTTG 2682
Qy 670 AATACAAATGATGATGATGATGCTTATTAATAATTTTATCCAGATGATATGAGCTTCA 729
Db 2683 AATGAAATATACAGAAATTTGGGTGATTTAAATTTCCGACAAACAAATGATATGCAACA 2742
Qy 730 GTAGGGAATCTAGAAATGATGATGAAAGAACCACTTAACAGGTGAACTTTGGCATGTG 789
Db 2743 CTAGGAATCTTGAATTTGTAAGAGAGGGGCACTTTGACGGGAAACATTGAACGAGCA 2802
Qy 790 AAACAAAGGAAAAAGAAATGGAACACACATGAGAAAAAAGCTTGGAAAAACACACAA 849
Db 2803 CAACAAACAAAGAAACAAATGCAAGACAAAAATGGCAAGAAAAAGTGGGCAATCGAAAAA 2862
Qy 850 GCCTATGATCGAGAAAAAGGCTGTGATGATCATTTATTAATAATGAACAAGATTACAC 909
Db 2863 GCATATTTATGCAAGAACCAAGCATGATGTTATTTGCGAGATTATCAAGAACCAAAA 2922
Qy 910 TATCATATTAATTTAGA-----TCATATTCAAAACGCTGATCGATGATGAT 963
Db 2923 CTTAATCTGTGTAAGAAATGTCAGATATGTTGGAGCCAAAACCTTGTACAGTCACTT 2982
Qy 964 CCTATGATATACATTAATTTGTTACCGAATGCTCAGGTATGAATGATATGATATCA 1023
Db 2983 CCTTACGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3042
Qy 1024 GAGTTAAACGACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
Db 3043 GAGTTAAACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3102
Qy 1084 AATGATGATTTTACACAGATTTACAGGATGACGACGACGACGACGACGACGACGACGAT 1143
Db 3103 AATGATGATTTTTCGAAATGATTAAGATTTGATGATGATGATGATGATGATGATGATGAT 3162
Qy 1144 CAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
Db 3163 CAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3222

Qy 1204 TTGCATGCTCAAGATCATCATGATATGTTAGTGTGATTTGGCAAAAAAGAGACCT 1263
Db 3223 TTTACATTTCAACCGAATTTATGATATGTTAGTGTGATGATGATGATGATGATGATGATGAT 3282
Qy 1264 GAAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
Db 3283 GGAACGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3342
Qy 1324 TCTTGCAGAAAG-----GATATGACAAAAACA 1353
Db 3343 ATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3402
Qy 1354 GTAGGATATTTCCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
Db 3403 GTGGAATTCATCTCATCTATACAGACAAAGTTGATTTGATTTGATGATGATGATGATGATGAT 3462
Qy 1414 TTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1454
Db 3463 TTCAACATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3503

RESULT 4
US-10-089-678-3
; Sequence 3, Application us/10089678
; Patent No. 6962977
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AND
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-089-678-3

Query Match 22.5%; Score 379; DB 3; Length 3690;
Bee Local Similarity 56.7%; Pred. No. 4.5e-86;
Matches 839; Conservative 0; Mismatches 555; Indels 87; Gaps 4;

Qy 22 AGTACGAAAAATACGTTAAATATGAAAAAGACAGATTTATGAAATAGATCAAGCGCCATT 81
Db 2248 AGTAAAAAAGATGCTTACAGACAGATGTAACGATTTATCAAGTATCAAGCGGCAAC 2307
Qy 82 TCTATGAAATGATGTCAGATGAAACAAATCTTCAAGAAAAAATATGTTATGGATGAA 141
Db 2308 TTATGTAATAGCTTATCGATGATGATTAATCCAAATGAAAAAGAAATGTTATGGATGCA 2367
Qy 142 ATAAAACGCGAAAAACAATTAGTGTGCTCGTAATCTTCCAAAAATGAGACTTTTCT 201
Db 2368 GTGAAAGGCGAAACGACTTGTTCAGGACGTAATCTTACCAAGATACAGGCTTTAAT 2427
Qy 202 GGGAAATGAT-----TGACATTCGGTAATGATTTATATGATGATCCAAATAT 249
Db 2428 AGGATTAATGAGAAAAAGCATGAGCGGGAAGTACGGAATTCGAGTTGGGAAAGAGAT 2487
Qy 250 CCTATTTTAAAGAAAAATTTCTACAGATGCGTGAGACGACGACATATATGAACTCTA 309
Db 2488 GTTCTGTTTAAAGATCGTTCGCTTCGTTTGAACAAGTGCAGAGAGATGATTAAGAAACA 2547
Qy 310 TTTCCAACTATATCTGTCAAAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 369
Db 2548 TATCCAAAGTATCTTATCAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2607

QY 370 CGAGTAAGAGGTTTGTGGAGTAAAGATTGAATTAATGTGTAACGCTACGGG 429
 DB 2608 AAACTAAAAGGTTTATAGGAAGTAGTCAGATTAGAGATTAAATTATACGTACGCG 2667
 QY 430 AAAAGAAATGATGCTATCATGAAATGTTCCAAATGATTTGGCCCTATATGACGCTATCCT 489
 DB 2668 GCAAAATCAAAATGCTCAAAAATGATACCAAGTAATCTCTTCCAGATGTATCCTCTGCAAT 2727
 QY 490 TCATGTGAGATTTATCGCTGTGAATCTCTCAATGTGATGTGAGCCAGGATATCTTACA 549
 DB 2728 TCTTGTGGGGATCGATCGATCGATGCAAGCAAGTAGT----- 2768
 QY 550 CCAACAGATGATGCTCCCATATGTATGATGCCCCCAAAATATAGTAGAAGCAT 609
 DB 2769 -----AGACGGGAATTTAGCACTCGAAAACATGAGAAAATGGA 2808
 QY 610 GTGAAGTGCAGATCGTATCATTTGATTTTCAATTTGACACCGGAGAGATGATACA 669
 DB 2809 AATATGCTCTTGTATCCATGCAATTTCTTCCATTTGATACAGGTAAATAGATTGG 2868
 QY 670 AATACAAATGATGATTTGATGCTTATTTAAATTTCTAATCCAGATGATACGCTACA 729
 DB 2869 AATGAAATATACAGGAATTTGGGCGATTTAAATTCGACAACAATGATACGCAACA 2928
 QY 730 GTAGGGAATCTGAAGTCAATTTGAAGAAGACCACTAACAGGTGAGCATTTGGCACAATG 789
 DB 2929 CTAGGAAATCTTGAATTTGTAGAGAGGGCCATTTGTCAAGGGGAAACATTAACACAGCA 2988
 QY 790 AAACAAAAGGAAAAGAAATGAAACAAACATGAGAGAAAACGTTGGGAAACACACACA 849
 DB 2989 CAACACAAAGAACACAAATGCGACACAAATGCGAAGAAAACGTGGGCACTACAGAAA 3048
 QY 850 GCGTATGATCCAGCAAAACAGGCTGTAGATGCAATTTATTAATGAAATGACAAAGTTAC 909
 DB 3049 GCATATTTATGAGCAAAAGCAATGTATCGTTATGCGAGATTATACAGCCAAA 3108
 QY 910 TATCATTTACTTTAGA-----TCATATTTCAAAAGCTGATGCACTGATACGTCGAT 963
 DB 3109 CTTAATTTCTGGGTGAGAAATGTCAGATATGTTGGCAGCCCAAAACCTTTGTACATTC 3168
 QY 964 CCGTATGATACCATTAATGTTGTACCGAATGCTCCAGATGATGATGATATATCA 1023
 DB 3169 CCTTACGRTATATATGATCGCTTACAGAAATCCCTGGAAATGATATACAGATTTTACA 3228
 QY 1024 GAGTTAAACGACGATATCATGCAAGGTTTAAATTTATATGATGCAAGAAATGTCATACA 1083
 DB 3229 GAGTTAAACAAATGATCTCCAAACAGATGGAATTTGTATGATCTTGAATGTATACCA 3288
 QY 1084 AATGTGACTTTTACACAGGATTTACAGGATGCGACGACACAGAAATCCCGCGTACA 1143
 DB 3289 AATGAGATTTTTCGAAATGATTAAGTGAATGCAACATCAAGATGTGATGTCACA 3348
 QY 1144 CAAATGATGAGGCTTCAATTAATGTTTATGATTAATTTGAAGGCGGGGATCTCAAAAC 1203
 DB 3349 CAACCTAGCGATACATCTGCTTGTCAATTCGAACTGGAATTTCAAGTGTCAACACA 3408
 QY 1204 TTGCAATGCTCAAGATCATGATGATATGTTTACGTTGATTTCCAAAAGAGAGACCT 1263
 DB 3409 TTTACAGTTTCAACCGAATTAATGATATGTTTACGTTGATGTCACAGCGAAGAGGAGTA 3468
 QY 1264 GGAAGAGGATATGTAAGATGATGATTTGTAATGGAAGCAGAAACATTTAAGTTCACT 1323
 DB 3469 GGAAGCGGATATGTAATGATTCGATGATGTCGAATCAGACAGAAACATCTCAATTAAT 3528
 QY 1324 TCTTGGCAAGAG-----GATATTTGACAAAACA 1353
 DB 3529 AATATGATGATGATACAGGTTTATATCTGCTGATCAAACTAGCTATATACAAAAACA 3588
 QY 1354 GTAGAGATTTCCACAGAAAGTATCGTGAACGATTTGAAATAGAGAAACCGAAGGTACA 1413
 DB 3589 GTGGAATTCATCTCATCTACAGAGCAAGTTTGGATTTGATGATGATGAGACCGAAGGTGTA 3648
 QY 1414 TTTTATATATGATGATCAAGTTGCTTTGTATGCAAGATA 1454

DB 3649 TTCAACATAGAAAGTGTAGAACTCGTGTATGAAAGAGAGTA 3689

RESULT 5
 US-07-915-203-1
 ; Sequence 1, Application US/07915203
 ; Patent No. 5359048
 ; GENERAL INFORMATION:
 ; APPLICANT: Ohba, Michio
 ; APPLICANT: Iwahana, Hidemori
 ; APPLICANT: Sato, Relichi
 ; APPLICANT: Suzuki, No. 5359048ukazu
 ; APPLICANT: Ogizawa, Katsutoshi
 ; APPLICANT: Sakanaoka, Kazunobu
 ; APPLICANT: Hori, Hidetaki
 ; APPLICANT: Amano, Shouji
 ; APPLICANT: Kawasugi, Tadaaki
 ; TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: US
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/915,203
 ; FILING DATE: 19920723
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: M/K 301
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3797 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bacillus thuringiensis
 ; STRAIN: japonensis
 ; INDIVIDUAL ISOLATE: Buihui
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 187..3636
 ; US-07-915-203-1

Query Match 21.2%; Score 357.4; DB 2: Length 3797;
 Best Local Similarity 56.8%; Pred. No. 1.4e-80;
 Matches 754; Conservative 0; Mismatches 516; Indels 57; Gaps 3;

QY 28 AAAAATAGCTTAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCAATTTCTATA 87
 DB 2233 AAAAGATGCTTACAGACAGAGTAAAGGATTATCAAGTCAATCAAGCGGCAAACTTATA 2292
 QY 88 GAATGATGTCAGATGAAACAAATCTCAGGAAAAATATATGTTATGAGTAAATTA 147
 DB 2293 GAATGCTATCCGATGAGAGATTATACCAATGAAAAAGAAATGTTATGAGATGCACTGAAA 2352
 QY 148 CTGGCAAAACAACTAGTCAAGTCTGTATATCACTCAAAATGAGAACTTTCTGGAAAT 207

Db 2353 GAGGCGAAGACGATTGTTACGGCAGTAACTTACTCAAGATACAGGCTTTAATAGATT 2412
Qy 208 GAT-----TGGACATTCGGTAATGATATATATCATAGATCCCAATATCTCTATT 255
Db 2413 AATGAGAAAAAGATGACGGGAAGTACGGGAATCGAGTTGTGAAAGAGATTTCTG 2472
Qy 256 TTTAAAGAAAAATTTCTACAGATGCGTGAGACAGACATATATGAACTCTATTTTCCA 315
Db 2473 TTTAAAGATCGTCCCTTCGTTTGACAAAGTCGAGAGATGATGATACAGAAAATATCCA 2532
Qy 316 ACTATATCTGTCAAAAAATAGATAGTCTAAATTTAAAAACCATATACAGTTATCGAGTA 375
Db 2533 ACGTATCTCTATCAACAATATAGATGAATCGCTTTAAAAACCATATACAAAGATATAACTA 2592
Qy 376 AGAGGTTTGTGGGAAGTAAAGATTTGAAATTAAATGCTAACCGTTACGGGAAAAA 435
Db 2593 AAAAGTTTAAAGAAAGTACAAAGATTTAGATTTAAATTAATCGTATCGGGCAAAAT 2652
Qy 436 ATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGACAGCTTAATCTCATGT 495
Db 2653 CAAATCGTCAAAAAATGTACAGATATATCTTTGCCAGATGACGCCCTGTCAATTTCTGT 2712
Qy 496 GGAAGTATTCGCTGTAATCATGCTCTCAGATATGTAGCGCAAGGTTATCTTACACCAACA 555
Db 2713 GGTGAGTTCGATCGCTGCAAGTGAACAAGATGTAGACGCAATTTAGCACTCGAAAAAC 2772
Qy 556 GATGATATGCTCCCGATATGATATGATGCCCGCAAAATATATAGATGAAGATGTGAAG 615
Db 2773 AATGAGAAAAATGAAAAATATGCTTCT----- 2799
Qy 616 TGTCAAGATCGTATCATTTGATTTTTCATATTTGACACCGGAGAGATGATCAATATACA 675
Db 2800 -----GATTCGCCATGCAATTTTCTTTCCATATGATGATACGGGTAATGATGAA 2853
Qy 676 AATGAGTATGATGCTTATTTAAAAATTTCTAATCAAGATGATGATGATGATGATGATGAT 735
Db 2854 AATACAGGAATTTGGATGCTGATTTTAAATTCGCAACAACAAATGAAACGCAACCTAGGA 2913
Qy 736 AATCTAAGATCATTTGAAGAAAGACCACTAACAGTGAAGATTTGGCACTGTGAAAAACA 795
Db 2914 AATCTGAATTTGTAAGAAAGAGGGGCAATTTGTCAGGGGAAACATTAAGATGGCCCAACA 2973
Qy 796 AAGGAAAAAATGGAACAACACATGGAAGAAAAACCTTGGGAAACAACAACAGCTAT 855
Db 2974 CAAGAAACAACATGTCAGCAAGCAAAATGCGAAGAAACCTGCAAGCATCAAGAAAAACATAT 3033
Qy 856 GATCCAGCAAAAACAGGCTGTAGATGATATTTTCAAAATGAACAAGTTACATATCAT 915
Db 3034 TATGACAGCAAAAGCAAGCATTTGATTCGAGATTTATCAAGACCAAAAACTTATAT 3093
Qy 916 ATTACTTTAGA-----TCATATTCAAAAAGCTGATGCACTGTGATCACTGCATTCCTCAT 969
Db 3094 TCTGCTGTGAAGAAATGTCAGATTTTGTGGACGCCCAAAACCTTGATCACTTCCTTTAC 3153
Qy 970 GTATATCTTAATTTGGTATACCGAATCTCCAGGTATGAACATAATGATATATCAAGATTA 1029
Db 3154 GTATATATGATGCTTACCGGAATCCCTGGAATGAACATAATGATTTTACAGAGTTA 3213
Qy 1030 AACGCACTATGCAAGAGTTATTAATTTATATGATGACGAATGTCAATAACAATGCT 1089
Db 3214 ACAATATACCTCAACAAGCATGGAATTTGATGATCTTCAAAACGCTATACCAATGGA 3273
Qy 1090 GACTTTACAAAGATTACAGGAGTGAACGCAACAGAAATGCCGCGTACAAACAATG 1149
Db 3274 GATTTTCGAATTTGAATTAAGTAAATTTGAATGCAACATGATTAATGTGCACAACTA 3333
Qy 1150 GATGAGCTTCAGTATGATTTCTATCAATTTGAGACGGGGGTATCTCAAACTTTGAT 1209
Db 3334 AGCGATATCATCTGCTCTGTCTATTCCAAACTGGAATTTCTCAAGTGTCAACAATTTTCA 3393
Qy 1210 GCTCAAGATCATCATGATATGTGTTTACGTGTGATTTGCCAAAAAAGAGACCTTGAAAA 1269
Db 3394 GTTCAACCGAATTTATGATATGTGTATGTCGTCAACAGGAGAAAAAGAGGAGTAGAGAC 3453

Qy 1270 GGGTATGTAACGATGATGATTTGATATGAAAGCAAGAAACATTAAGTCACTTCTGC 1329
Db 3454 GGATATGATCATTCCTGATGTCGATGTCAAATCATGACAGAAACATCACTTAATATATGT 3513
Qy 1330 GAAGAG 1336
Db 3514 GATGATG 3520
RESULT 6
US-08-272-887-1
; Sequence 1, Application US/08272887
; Patent No. 5747450
; GENERAL INFORMATION:
; APPLICANT: Onda, Michio
; APPLICANT: Iwanana, Hidemori
; APPLICANT: Sato, Reichi
; APPLICANT: Suzuki, No. 5747450kazu
; APPLICANT: Ogiwara, Katsutoehi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasaki, Tadaaki
; TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,887
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: japonensis
; INDIVIDUAL ISOLATE: Bulbul
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3636
; US-08-272-887-1
Query Match 21.2%; Score 357.4; DB 2; Length 3797;
Best Local Similarity 56.8%; Pred. No. 1,4e-80;
Matches 754; Conservative 0; Mismatches 516; Indels 57; Gaps 3;
Qy 28 AAAAAATCGTTAAATATGAAGACAGATTTATGAAATATGATCAAGCGCCATTTCTATA 87

Db 2233 AAGATGCTTACAGACAGTAAACGATTTATCAAGTCATCAAGCGCAAACTTAATA 2292
Qy 88 GAATGATGTCAGATGAACAAAATCTCAGAAAAAATATGTTATGGGATGAATAAAA 147
Db 2293 GAATGCTATCCGATGAGTTATACCAATGAAAAACGAATGTTATGGGATCAGTGAAA 2352
Qy 148 CTGGCAAAACCACTTATGTCAGTCTGTTATCTACTCCAAATGAGACTTTTCTGGGAAT 207
Db 2353 GAGGGAAAACGACTGTTCCAGGACGTAACTTACTCCAGATACAGGCTTTTATAGGAT 2412
Qy 208 GAT-----TGACATTCGGTAAATGATATATATCATGAGATCCAAATATCTAT 255
Db 2413 AATGAGAAAACGATGAGCGGAAAGTACGGAAATCGAGGTGTGGAGAGAAATGTTCTG 2472
Qy 256 TTTAAAGAAAAATTTCTACAGATGCGTGAGACAGACATATATGAACTCTATTTTCCA 315
Db 2473 TTTAAAGATCGTTGCTTCTGTTGAAGAATGCGAGAGATGATATACAGAAACATATCCA 2532
Qy 316 ACCTATATCTGCACAAAAATAGATAGTCTAAATTTAAACCATATACAGTTATGAGTA 375
Db 2533 ACGTATCTCTATCAACAAATAGATGATCGCTTTAAACCATATACAGATATTAACCTA 2592
Qy 376 AGAGGTTTGGGAAAGTAAAGATTGAATTAATGTTAAACGTTAAGCGGAAAGAA 435
Db 2593 AAAAGTTTATAGAAAGTATGACAGATTTAGATTAATTAATATGCTATCGGCAAAAT 2652
Qy 436 ATTGATGCTATCATGATGTTCCAAATGATTTGGCTATATGACAGCTTATCTTCAATG 495
Db 2653 CAATGCTCAAAAATATGACAGATATATCTTGGCAGATGTAAGCGCTGTCAATTTCTGT 2712
Qy 496 GGAGATTATCGCTGATCATGCTCTCAGTATGAGCGCAAGGATTCATACACCAACA 555
Db 2713 GGTGAGTCGATGCGTGCAGTGAACAACAGTATGTAGACGCAATTTAGCAGTCAAAAAC 2772
Qy 556 GATGATATGCTCCGATATGATGATGATGCGCGCAAAATATGATGAAGAAGATGTGAAG 615
Db 2773 AATGAGAAAATGAAAATATGCTCTT----- 2799
Qy 616 TGTCAAGATCGTCATCATTTGATTTTTCATATTTGACACCGGAAAGTATGATCAAAATACA 675
Db 2800 -----GATTCAGATGATTTTCTTTCATATTTGATTAAGGGAATATGATTTGATGAA 2853
Qy 676 AATGATGATTTGATGCTTATTTAAATTTTCTAATCCAGATGATGCTTACAGTAGGG 735
Db 2854 AATACAGGAATTTGATGCTATTTAAATTTCCAGAACAAATGGAACCCCAACACTAGGA 2913
Qy 736 AATCTAGAATGCTTGAAGAAGACCACTAACAGGTGAAGCTTTGGCAATGTGAACA 795
Db 2914 AATCTTGAATTTGTAGAAAGAGGGCCATTTGCAAGGGAACATTTAGAAATGGGCCCAACAA 2973
Qy 796 AAGAAATAGAAATGGAACCAACATGAGAAAAAAGCTTTGGGAAACCAACAGAGCTTAT 855
Db 2974 CAAGAACCAACATGCGACAGAACAAATGCGAAGAAAACGTGCAATCAGAAAAAACATAT 3033
Qy 856 GATCCAGCAAAACAGGCTGTAGATGATTTTAAATGAACAAAGTTACATCATATCAT 915
Db 3034 TATGACAGAAAGCAAGCATGATGATTTATTCGCAAGATATCAAGACCAAAAACCTTAT 3093
Qy 916 ATTACTTTAGA-----TCATATTCAAAACGCTGATCGCTGTCAGTGCATTCCTAT 969
Db 3094 TCTGGTGTAGAAATGTCAAGATTTGTTGGAGGCCCAAAACCTTGTACAGTCCATTCCTTAC 3153
Qy 970 GTATACCATTAATTTGGTTACCGAATGCTCCAGGTATGAACTATGATATATCAAGTTA 1029
Db 3154 GTATATATATGATGCTTACCGAAATCCCTGGAATGAATTAACAGATTTTACAGGTTA 3213
Qy 1030 AAAGCACTATCATGACAGCTTATTAATTTATATGATGACAGAAATGCTAAACAAATGCT 1089
Db 3214 ACAAAATAGACTCAACAGCATGAAATTTGTATGATCTTCAAAACGCTTATACCAATGGA 3273
Qy 1090 GACTTTACAGAGATTAAGGAGATGCGACGAAACGAAATGCGCGGTACAAACAAATG 1149

Db 3274 GATTTGCAAAATGATTAAGTAATTTGATGACCAATCATGATGTAATGTGCAACACTA 3333
Qy 1150 GATGAGCTTACAGTATTAATTTCTATCAAAATGAGCGGGGGTATCTCAAACTTGAT 1209
Db 3334 AGCGATACATCTGTCCTTGTATTCACAACTGGAATTTCTCAAGTGTCAACAAATTTCA 3393
Qy 1210 GCTCAAGATCATGATGATGTTAGTGTAGTGTGATTCGCAAAAAGAGAACCTGGAATA 1269
Db 3394 GTTCAACCGAATTAATGATATGTTGTTACGTTACAGACGAGAAAGAGGAGTAGAGAC 3453
Qy 1270 GGGTATGTACAGATGATGATTTGTAATGAAAAAGCAGAAACATTAAGTTCACTTCTGC 1329
Db 3454 GGATATGTATCATCTCGATGATGTCGAATATGACAGACAGAAACACTCAATTTAATATGT 3513
Qy 1330 GAGGAG 1336
Db 3514 GATGATG 3520

RESULT 7
US-08-789-449-1
; Sequence 1, Application US/08789449
; Patent No. 5824878
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwahana, Hidemori
; APPLICANT: Sato, Relichi
; APPLICANT: Suzuki, No. 5824878ukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakana, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Amano, Shouji
; APPLICANT: Kawasugi, Tadaaki
; TITLE OF INVENTION: No. 5824878el Microorganism and insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,449
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,887
; FILING DATE: 08-JUL-1994
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: japonensis

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INDIVIDUAL ISOLATE: Bulbul
FEATURE:
NAME/KEY: CDS
LOCATION: 187..3636
US-08-789-449-1

Query Match      21.2%; Score 357.4; DB 2; Length 3797;
Best Local Similarity 56.8%; Pred. No. 1.4e-80;
Matches 754; Conservative 0; Mismatches 516; Indels 57; Gaps 3;

Qy 28 AAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCACTTTCTATA 87
Db 2223 AAAAGATGCTTACACAGACAGTGTAAACGATTATCAAGTCAATCAAGCGGCAAACTTAATA 2292
Qy 88 GAATGATATGTCAGATGAAACAAATCTCTCAGGAAAAATTAATGTTATGGGATGAATATAA 147
Db 2293 GAATGCTTATCCGATGAGTTTATACCAATATGAAAAACAAATGTTATGGGATGCACTGAAA 2352
Qy 148 CTGGCAAAACAACTAGTCTGCTATCTACTCCAAAATGGAGCTTTTCTGGGAA 207
Db 2353 GAGGCGAAACGACTTGTTCAGGACGTTAACTTCTCCAAAGATACAGGCTTTTATAGGAAT 2412
Qy 208 GAT-----TGGACATTCGGTAAATGATATATCATAGATCCAAATATCTAT 255
Db 2413 AATGAGAAACGATGACGGAAGTACGGAATCGAGTTGTGAAGAGATGTTCTG 2472
Qy 256 TTTAAAGAAAAATTTCTACAGATGCGTGAGACAGACATATATGAACTTATTTCCA 315
Db 2473 TTTAAAGATCGTTCCTTCGTTTGACAAATGCGAAGATGATGAAACAAATATCCA 2532
Qy 316 ACCTATATCTGTCAAAAAATAGATGATCTAAATTAACCAATATACAGTTATCGAGTA 375
Db 2533 ACGTATCTCTATCAACAAATAGATGATATCGCTTTAAACCAATATACAGATATATACTA 2592
Qy 376 AGAGGTTTGGGGAAGTAGTAAAGATTGAATTAATGTAAACAGTTACGGGAAAGAA 435
Db 2593 AAAGGTTTATAGGAAGTAGTCAAGATTAGAGATTAATTAATGATCGTATCGGCAAT 2652
Qy 436 ATTGATGCTATCATGATGTTCCAAATGATTTGGCTATATGCAAGCTTATCTTCAAT 495
Db 2653 CAAAATCGCAAAATATGACCAAGATATCTCTTGCAATGTAACGCTGTCATCTTGT 2712
Qy 496 GGAAGTATCGCTGTCGATCATCTGCTGATATGAGCCAAAGGTTATCTTACACCAACA 555
Db 2713 GGTGAGTCGATCGCTGCAAGTGAACAACGATATGAGCGGAATTTAGCACTCGAAAC 2772
Qy 556 GATGATATGCTCCCGATATGATGATGCCGCAAAATATAGATGAAGAAGCATGTAAG 615
Db 2773 AATGGAGAAATATGAAATATGCTCT----- 2799
Qy 616 TGTACAGATCGTCACTTTGATTTTTCATATATGACACCGGAGAAATGATACAAATACA 675
Db 2800 -----GATTCCTCAATGATTTTCTTTCATATGATGAGGGGAAATGATTTGATGAA 2853
Qy 676 AATGATGATTTGATGATGTTTATTAATAAATTTCTAATCCAGATGATGATGATGATGAG 735
Db 2854 AATACAGGAATTTGATGATGATTTTAATAATTCGACAAATGATGAACGCAACACTAGGA 2913
Qy 736 AATCTGAAGTCAATTGAAGAAGACCACTAAACAGTGAAGCATTTGGCACTGTGAAACAA 795
Db 2914 AATCTGAATTTGATGAAGAGGGGCACTTGTCAAGGGGAAACATTTGAATGGGCCAACAA 2973
Qy 796 AAGGAAAAAATGAAACCAACACATGAGAAAAAAGTTGGGAAACCAACAGCCAT 855
Db 2974 CAAGAAACAATGCAAGCAAAATGCAAGAAAACTGACGATTCGAAAAAACATAT 3033
Qy 856 GATCAGCAAAACAGGCTGATGATCATTTATTAACAAATGAACAAGATTCACATATCAT 915
Db 3034 TATGACGAAAGCAAGCATGATGATTTTATTCGAGATTTATCAAGACCAAAATCTTAAT 3093
Qy 916 ATTACTTTAGA-----TCATATTTCAAAACGCTGATCAGTGTACAGTGTCCCTAT 969
Db 3094 TCTGTGTGAAGAAATGTCAGATTTGTTGGCAGGCCAAAACCTTGTACAGTCTCTTAC 3153
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Qy 970 GTATACCAATATTTGGTTACCGAATGCTCCAGGTATGAATGATATATCAAGAGTTA 1029
Db 3154 GTATATATATGATGCTTACCGGAATCCCTGGAATGAATCTATACAGATTATACAGAGTTA 3213
Qy 1030 AACCCAGTATCATGACGAAGTTATTAATTTATATGATCAGCAAAATGTCATTAACAAATGCT 1089
Db 3214 ACAAAATGACTCCAAACAAGCATGGAATTTGATATCTTCAAAAACGATATCCAAATGGA 3273
Qy 1090 GACTTTACACAAGATTTACAGGATGCGACCGCAACAGAAATGCCGGGTACAACAATG 1149
Db 3274 GATTTTCAAAATGATTAATGATTAATGGAATGCAACATCAGATGTAATGTCACAACTA 3333
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Qy 1210 GCTCAAGATCATCATGATATGTTTACGTTGATTCACAAAAAAGAAAGACCTGGAATA 1269
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Qy 1270 GGGTATGTAACGATGATGATGTTTAATGAAAGCAAGAACATTTAAGTTCACTTCTTGC 1329
Db 3454 GGATATGATCATCTCGATGATGTCAAATCAGACAGAAACATCATTAATTAATATGT 3513
Qy 1330 GAAGAAG 1336
Db 3514 GATGATG 3520

RESULT 8
US-07-876-280-29
Sequence 29; Application US/07876280
Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158e1 Bacillus thuringiensis Isolates for
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESS: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILING DATE: 19970430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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ORIGINAL SOURCE:
ORGANISM: *Bacillus thuringiensis*
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
CLONE: E. coli NMS22 (pMVC2320) NRRL B-18769
US-07-876-280-29

Query Match 18.5%; Score 311.8; DB 2; Length 3471;
Best Local Similarity 55.6%; Pred. No. 4.8e-69;
Matches 815; Conservative 0; Mismatches 547; Indels 105; Gaps 7;

22 AGTACGAAATACGTTAAATATAGAACGACAGATTTATGAATATGATCAACGGCCATT 81
DB AATACAAAAGATGCGTTACGACAGAGTGTACGAGTTATGAATTAACCGGCAAC 2109
82 TCTATAGATGTATGTACAGATGACAAATCTCAGAAAATAATATGTTATGGATGA 141
DB TTATAGGATGCTTATCGATGATTTATATCCAAATGAAAAAGATTTATTTATGATCG 2169
142 ATAAACTGGCAAAACAACTTAGTCACTCGTAATCTCACTCAAAATGAGACCTTTCT 201
DB GTAGAGAGGCAAAACGCTCGAGGCGACGTAACCTTACTCAAGATCCAGATTTCCAA 2229
202 GGG-----AATGATTGACATTCGGTATGATTTATCTATAGATCCAAATAT 249
DB GAGATTAACGAGAAATGATGAGGCGGCAAGTACGGGAATTGAGATTGAGAGGGGAT 2289
250 CCTATTTTAAAGAAATTTCTACAGATGCGTGAGAGACGACATATATGAACTCTA 309
DB GCTGATTTAAAGACGTTATCTACGCCCTACAGGTGCGACGAAATTTATACGAAACG 2349
310 TTTCCAACTTATCTGTCAAAAAATAGATGAGTCTAAATTAATTAACCATATACAGTTAT 369
DB TATCCAACTGATCTGATCAAAAAATAGAGAGAGGATGATTAACCATATACAGATAT 2409
370 CGAGTAAGAGGTTTGTGGAGATGATGAATTTGAATTAATGATACAGTTACGGG 429
DB AGACTGAGAGGGTTGTGGAGATGATCAAGATTTAGAAATTTATACGATACGCTCAC-- 2466
430 AAAGAATTTGATGCTATCATGATGATGTTCCAAATGATTTGGCGCTATATGACGCTATCCT 489
DB CAAGCAATGCAATTTGTAAAGATGTACCAAGTATTTA----- 2505
490 TCATGTGAGATTTATCGCTGTAATCATGCTCATGATGTAGAGCCAGAGGATCTCTACA 549
DB -TTGCCAGATGATCTCTGTAACCTGATGCGAGTAT-----CAATCGATGACGGCA 2558
550 CCAACGATGATGATGCTCCGATATGATGATGCGCCGCAAAATTTAGATGAAGAAT 609
DB ACAAAGATGATGATGATGCGGTTTAGAGAGAAAAACCG----- 2597
610 GTGAAGTGCACATGCTATCATTTGATTTTCAATTTGACACGGGAGAGATGATGATACA 669
DB -----TTCTGCTGATGACATGATTTCTGCTCCCTATGATATGAGAGCTGATATAC 2652
670 AATACAAATGTATGATGATGATGCTTATTTAAATTTCTAATCCAGATGATGATGATACA 729
DB AATGAATATGACGAATATGAGGTTGATTTAAGATTAAGGAGCCAGAGGATATCGAATA 2712
730 GTAGGAATCTTGAAGTCACTTAAGAAGACATTAACGGTGAAGCATTTGCAACATGTG 789
DB CTGGAATCTTGAATGATGATGAGGAGGACCTTTGTCAAGAGACGATTTAAGCGCTTG 2772
790 AAAAGAAAGAAAGAAAGAAACAAACATGAGAGAAAAAGTTGGGAAACACAAACA 849
DB CAAAGAGAAAGAAACAGTGAAGATTCAAATGACAAAGAGCGTGAAGAGACAGATAGA 2832
850 GCTTATGATCGACAAACAGGCTGATGATTTATTTCAATGAACAAAGATTTACAC 909
DB AGATACATGATCGACAAACAGGCGGATGATGATTTATGATGATGATGATGATCAACA 2892
910 TATCATATTACTTTATGATGATATA-----TTCAAAACGCTGATGATGATGATGAT 963

DB CTGAATTCCTGATGTAGATTTACAGATCTTACTGCGGCTCAAGATTTGATACATTCATT 2952
964 CCTATGATATACCAATTTGTTTACCAATGCTCAGAGTATGATGATGATGATGATCA 1023
DB CCTTATGATATTAAGAAATGTTTCCAGAAATATACAGGATGATGATGATGATGATCA 3012
1024 GAGTTAAACGACGATATCATGCAAGTTATTAATTTATGATGACAGAAATGCTATACA 1083
DB GAATTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3072
1084 AATGATGATTTTACCAAGATTTACAGGATGATGATGATGATGATGATGATGATGATGAT 1143
DB AATGATGATTTTACCAAGATTTTACAGGATGATGATGATGATGATGATGATGATGATGAT 3132
1144 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
DB CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3192
1204 TTGATGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
DB TTGATGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3252
1264 GGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
DB GGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3312
1324 TCTTTCG-----AAGAGATATATGACAAACAA 1353
DB GCAAGCAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3372
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DB GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3432
1414 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3459

RESULT 9
US-07-812-180A-1
; Sequence 1, Application US/07812180A
; Patent No. 5366892
; GENERAL INFORMATION:
; APPLICANT: Fonzecada, Luis R
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
; TITLE OF INVENTION: Thuringiensis Isolate and a No. 5366892el Gene Encoding a
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roman Saliwanchik
; STREET: 2421 N.W. 41st Street, Ste A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/812,180A
; FILING DATE: 19920102
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800

```

; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 3471 base pairs
;     TYPE: NUCLEIC ACID
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;     ORGANISM: Bacillus thuringiensis
;     STRAIN: kumamotoensis
;     INDIVIDUAL ISOLATE: PS50C
;   IMMEDIATE SOURCE:
;     LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF LUIS
;     LIBRARY: FONCERRADA
;     CLONE: 50C
;   US-07-812-180A-1

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Query Match      18.5%; Score 311.8; DB 2; Length 3471;
Best Local Similarity 55.6%; Pred. No. 4,8e-69;
Matches 815; Conservative 0; Mismatches 547; Indels 105; Gaps 7;

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QY 22 AGTACGAAAATACGTTAAATAGAAAAGACAGATTATGAAATAGATCAAGCGGCATT 81
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QY 82 TCTATAGATGTATGTCTAGATGAACAATACTCTCGAGAAAAAATATGTATGGATGAA 141
DB 2110 TTAGTGAATGCTATTCGATGATTTATATCCAAATGAAAAACGATTGTTATTTGATGCG 2169
QY 142 ATAAACCTGGCAAAACCACTTAGTCACTCTGTAATCTACTCCAAATGAGACTTTTCT 201
DB 2170 GTGAGAGGCGAAAACGCTCAGTGGGCGAGTAACTTACTACAGATCCAGATTTCCAA 2229
QY 202 GGG-----AATGATTGACATTCGGTAATGATTTATTCATAGATCCAAATAT 249
DB 2230 GAGATTAACGAGAAAATGATGAGGCGGCAAGTACGGAATTGAGATTGAAAGGGGAT 2289
QY 250 CCTATTTTTAAAGGAAAATTTCTACAGATGCGTGAAGACAGACATATATGGAATCTTA 309
DB 2290 GCTGATTTTAAAGGCGTTATCTACGCTTACCGAGTGCAGAGAAATTTGATACGGAACG 2349
QY 310 TTTCCAACTTATCTGTCAAAAATAGATGAGTCTAAATTTAAACCATATACAGCTTAT 369
DB 2350 TATCCAACTATCTGTATCAAAAAGTATAGAGAGAGTGTATTTAAACATACACAGATAT 2409
QY 370 CGAGTAAAGGGGTTTGGGAAAGTAAAGATTGAATTTAATGTTAAACGTTACGCG 429
DB 2410 AGACTGAAGGGGTTTGTGGAAAGTGTCAAGGATTAGAAATTTATACATACGTAC--- 2466
QY 430 AAAAAGATGATGCTATCATGAAATTTCCAAATGATTTGGCGCTATATGACAGCTTATCT 489
DB 2467 CAACGAAATCGAATTTGTAAGAAATGTATCAAGATGATTTA----- 2505
QY 490 TCATGTGAGAGATTTATCGCTGTGAATCATCGTCTCAGTATGAGCCAGAGGATCTTACA 549
DB 2506 -TTGCCAGATGTATCTCTGTAAACTGTAGTGGCAGTAT-----CAATCATGACAGCA 2558
QY 550 CCAACAGATGATATGCTCCCGATATGTATGATGATGATGATGATGATGATGATGAT 609
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QY 610 GTGAAGTCTCAGATCGTATCATCTTAAATTTCTATATGACACCGAGAAATGATGATGAT 669
DB 2598 -----TTCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2652
QY 670 AATACAAATGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
DB 2653 AATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2712
QY 730 GTAGGGAATCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789

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DB 2713 CTGGAATCTTGAATTAATGTCGAAAGAGGACCTTTGTCAAGAGACGATTAGAGCGCTTG 2772
QY 790 AAAAAGAGAAAAGAAATGGAACCAACACATGAGAAAAGAAAGCTTGGAAACACACAA 849
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QY 850 GCTATGATCCAGCAAAACAGGCTGTATGATGATGATGATGATGATGATGATGATGAT 909
DB 2833 AGATACATGCGATGGAACCAAGCGTATGATGATGATGATGATGATGATGATGATGAT 2892
QY 910 TATCATTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
DB 2893 CTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2952
QY 964 CCCATGATATACCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023
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QY 1024 GAGTTAAACGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
DB 3013 GAATTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3072
QY 1084 AATGATGATTTTACCAAGATTTACAGGATGATGATGATGATGATGATGATGATGATGAT 1143
DB 3073 AATGATGATTTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3132
QY 1144 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
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QY 1204 TTGCATGCTCAAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
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DB 3373 GTGACATTTCAATCCGATTAACAGATCAATGTGATTTAAATTAATGATGAAACGAAAGTACG 3432
QY 1414 TTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 3433 TTTTATATGAAAGTGTAGAAATGATTT 3459

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RESULT 10
US-08-315-468-1
; Sequence 1, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
;   APPLICANT: Michaels, Tracy Ellis
;   APPLICANT: Foncerra, Luis
;   TITLE OF INVENTION: Process for Controlling Scarab Pests
;   TITLE OF INVENTION: with Bacillus thuringiensis Isolates
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: David R. Salivanchik
;     STREET: 2421 N.W. 41st Street, Suite A-1
;     CITY: Gainesville
;     STATE: FL
;     COUNTRY: USA
;     ZIP: 32606
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwahchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF LUIS
LIBRARY: FONCERBADA
CLONE: 50C(a)
US-08-315-468-1

Query Match 18.5% Score 311.8; DB 2; Length 3471;
Best Local Similarity 55.6%; Pred. No. 4,8e-69;
Matches 815; Conservative 0; Mismatches 547; Indels 105; Gaps 7;

QY 22 AGTACGAAATATAGCTTAAATAGAAAGACAGATTATGAATAGATCAGCGCCATT 81
DB 2050 AATACAAAGATGCTTACGACCAAGTGTAAACGATTTATGAATCAACCGCAAC 2109
QY 82 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
DB 2110 TTATGGAATGCTTATCGATGATTTATATCCAAATGAAACGATGTTATTTGATGCG 2169
QY 142 ATAAAGTGGCAAAACAATTAGTCAAGTCTCGTAATCTCAAAATGAGACTTTTCT 201
DB 2170 GTGAGAGGCAAAACGCTTCCGTTGGGCACTTAATCTCAAGATCCAAATTTCCA 2229
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QY 370 CGAGTAAAGGTTTGTGGAGATGATAAATTTGAAATTAAGTAAACACGTTACGGG 429
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QY 430 AAGAAATTTGATGCTATCATGATGTTCCAAATGATTTGGCCTATATGACGCTAATCT 489

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QY 490 TCATGTGAGATTTATCGTGTGAATCATGCTCTCAATGTGAGCCAAAGGTATCTTACA 549
DB 2506 -TTGCCAGATGATCTCTGTAAACTGTATGCGCAGAT-----CAATCATGACAGCA 2558
QY 550 CCACAGATGATATGCTCCCGATATGATGATGATGATGATGATGATGATGATGATGAT 609
DB 2559 ACMAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2597
QY 610 GTGAAGTGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
DB 2598 -----TTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2652
QY 670 AATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
DB 2653 AATGAAATGACAGAAATGAGGTTGATTTAAGATTACGACCCGAGAGGATACCAACA 2712
QY 730 GTAGGATCTGAAAGTATGAAAGAACCACTAACAGGTGAAGCATGSCATGTG 789
DB 2713 CTGGAAATCTGAAATTAAGTGAAGAGGACCTTGTGAGAGACGCAATGAGCGCTTG 2772
QY 790 AAACAAAGAAAGAAATGAAACAAACATGAGAGAAACGTTGGGAAACAAACAA 849
DB 2773 CAAGAGAAAGAAACAGTGAAGATTTCAATGACAAAGACGTAAGAGACAGATAGA 2832
QY 850 GCCTATGATCCAGCAAAACAGCTGTAGATCATTATTACAAATGAACAAAGATTACAC 909
DB 2833 AGATCATGATGATGAAACAAAGCGGTAGATGTTATATGCGGATATACAGATCAACA 2892
QY 910 TATCATATTAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
DB 2893 CTGATCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2952
QY 964 CCTATGATATCAATATTTGTTTACCAAGTCTCAGGTATGAACTATGATGATGATGAT 1023
DB 2953 CTTTACGATATTAAGAAATGTTTCCAGAAATACAGGATGAACTATACGAAGTTTACA 3012
QY 1024 GAGTTAAACGACGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
DB 3013 GAATTAACAGATTCAGCTCAACAAAGCTGATGATGATGATGATGATGATGATGATGAT 3072
QY 1084 AATGTGATTTTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
DB 3073 AATGTGATTTTTCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3132
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QY 1204 TTGATGCTCAAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
DB 3193 TTTACAGTTCAACGAAATCAAAAGATATGATATTAAGATTTACGCAAGAAAGGAGTA 3252
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DB 3433 TTTTATATGAAAGTGTGAAATTTGAT 3459

RESULT 11
US-07-941-650A-1

Sequence 1, Application US/07941650A
Patent No. 6294184
GENERAL INFORMATION:
APPLICANT: Uyeda, Kendrick A.
APPLICANT: Bradisch, Gregory A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,650A
FILING DATE: 19920908
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,935
FILING DATE: 21-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,112
FILING DATE: 16-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Bacillus thuringiensis*
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC1638), NRRL B-18751
US-07-941-650A-1

Query Match 18.5% Score 311.8: DB 3: length 3471;
Best Local Similarity 55.6% Pred. No. 4.8e-69;
Matches 815; Conservative 0; Mismatches 547; Indels 105; Gaps 7;

QY 22 AGTACGAAATAATACCTTAAATAAGAAAAGACAGATTATGAAATGATCAAGCGGCCTATT 81
DB 2050 AATACAAAAGATGCGTTACGACCGAGGTGAACGATTTATGAAGTAAATCAAGCGGCACAAC 2109
QY 82 TCTATGATGATGATGTCAGATGAGACAAATCTCTCAGAAAAAATATATGTTATGGATGAA 141
DB 2110 TTAGTGAATGCTATTCGATGATTTATATCCAAATGAAAAACGATGTGTATTTGATCG 2169
QY 142 ATAAACAGGCAAAACAACTTAGTCAGTCTGATATCTACTCCAAATGGAAGCTTTCT 201
DB 2170 GTGAGAGGCAAAACGCTTCAGTGGGACGTAACCTTACTACAAAGATCCAGATTTCCA 2229
QY 202 GGG-----AATGATTGACATTCGGTATGATATTTATCATAGATCCAAATAT 249

DB 2230 GAGATAAACGGAGAAAATGATGGCGGCAAGTACGGGAATTGAGATTGTGAAGGGAT 2289
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DB 2250 TATCCAGATATCTGTATCAAAAAGTAGAGAGAGTATTTAAACCATACACAGATAT 2409
QY 370 CGAGTAAAGAGGTTTGGGAGAGTAGTAAAGATTGAATTTAATGTAAACGTTACGGG 429
DB 2410 AGACTGAGAGGGTTTGGGAGAGTAGTCAAGATTGAATAATTTATACGATCGTCAC-- 2466
QY 430 AAAAATTTGATGCTATCATGAAATGTTCCAAATGATTTGGCCTATATGACGCTTAATCCT 489
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QY 490 TCATGTGAGATTAATCGCTGGAATCATCGTCTCAGTATGTGAGCCAAAGGTTATCTTACA 549
DB 2506 -TTGCCAGATGATATCTCTGTAACTGTATGCGAGTAT-----CAATGATGACAGCA 2558
QY 550 CCAACAGATGATATGCTCCGATATGTATGATGATGCGCCGCAAAATATATGATGAAGCAT 609
DB 2559 ACAAAGATATGATGATGACCGTTTGAAGAGAAACCG----- 2597
QY 610 GTGAAGTGTACGATTCGTATCCATTGATTTTATATATGACACCGGAGAGTATGATACA 669
DB 2598 -----TTCTGTGTATGACATGAGATTCGCTCCCTATCAATATGAGAGAGCTGATTAAC 2652
QY 670 AATCAAAATGATGATTTGATGATGCTTATTAATAATTTCTAATCCAGATGATATGATCTACA 729
DB 2653 AATGAATATGAGAAATATGAGTTGATTTAAGTTACGAGCCAGAGGATATGCAACA 2712
QY 730 GTAGGGAATCTGAAGATCATTTGAAGAAAGCACTAAACGTTGAAGCATTTGGCATGTG 789
DB 2713 CTGGAATCTTGAATTAATGTCGAAGAGGACCTTTGTACGAGACGATTTAGACGGCTTG 2772
QY 790 AAACAAAAGAAAAGAAATGGAACACACATGAGAAAACGTTGGGAAACACACAA 849
DB 2773 CAAGAGAGAAACAAACGATGAAATTCMAATGCAAGAAACGTAAGAGACAGATGAGA 2832
QY 850 GCTATGATCCAGCAAAACAGGCTGTAGATCATTTTACAAATGCAACAGATTACAC 909
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QY 910 TATCATATTAATCTTAGATCATTA-----TTCAAAACGCTGATGCTGTATCAGTCAAT 963
DB 2893 CTGAATCCTGATGTAGAGATTAACAGATCTTACTCGGCTCAAGATCTGATCAGTCAAT 2952
QY 964 CCTATGATATCAATTAATGTTTACCGAATGCTCCAGATGAACTATGATGATATCA 1023
DB 2953 CTTACGATATTAACGAATGTTTCCAGAAATACAGAGATGAACTATACGAAGTTTACA 3012
QY 1024 GAGTTAAACGACGATATCATGACAAAGTTATATTTATATGATGACAGAAATGTCATACA 1083
DB 3013 GAATTTACAGATTCATCTCAACAGCGTGAATTTGATATGATCGCAAAATGCAATACA 3072
QY 1084 AATGTGACTTTTACACAAAGATTACAGAGATGCAACGCAACAGAAATGCCGCGTACAA 1143
DB 3073 AATGTGATTTTCAAAATGGGTTAAGTAATGGAATCAACGCTCGGTGAGAGTTCAA 3132
QY 1144 CAATGATGAGAGTTCAATGTTTATGTTCTATCAAAATGAGAGCGGGGGGTATCTCAAAC 1203
DB 3133 CAATCAATCAATATATCTGCTTGTATTTCCAAACGAGGATGAAACAAGTTTCAACAAG 3192
QY 1204 TTGATGCTCAAGATTCATATGATGATGTGTTTACGTTGATGTTGCCAAAAAGAGAGCCT 1263
DB 3193 TTTTACAGTTCAACGAATCAAAAGTATGTATTTACGATTTACTGCAAGAAAAGAGGGGTA 3252
QY 1264 GAAAAGAGGATGTATACGATGATGATTTGTAATGAAAAGCAGAAACCTTAAGTTCACT 1323
DB 3253 GGAATGATATATGTAAGTATTCGTGATGTGGAATATCAATCAGAAACGCTTACTTTAGT 3312

QY 1324 TCTTCG-----AAGAGATATATGACAAACAA 1353
DB 3313 GCAACCGATTATGATACAAATGCTGTATTAATGACCAACCGGCTATTCACAAACAA 3372
QY 1334 GTAGAGGATTTCCGAAAGATGCTGTAGAGATTGAATGAGAAACGAGGTGCA 1413
DB 3373 GTGACATTCATCCCGTATACAGATCAAAATGTGATTGAATATAGTAACAGAGGTACG 3432
QY 1414 TTTTATATAGATAGCATCGAGTTGCTT 1440
DB 3433 TTCTATATAGAAAGTGTAGATTGATT 3459

RESULT 12
US-07-973-320-3
; Sequence 3, Application US/07973320
; Patent No. 5286486
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Fu, Jenny M.
; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanichik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,320
; FILING DATE: 19921106
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/788,638
; FILING DATE: 6-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanichik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA68.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3414 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: HD867
; IMMEDIATE SOURCE:
; LIBRARY: Lamdagem (TM)-11 library of J.M. Fu
; CLONE: 867
US-07-973-320-3

Query Match 18.0%; Score 303; DB 2; Length 3414;
Best Local Similarity 53.5%; Pred. No. 8.1e-67;
Matches 784; Conservative 0; Mismatches 600; Indels 81; Gaps 4;

QY 28 AAAAATCGTTAAAAATGAAAGACAGCATTTATGAAATGATCAAGCGCATTTCTATA 87

DB 1991 AGAAATGCACTCCAAAAAGACCTGACAGATTATTAAGTGACAGGTTTCAATTTTACTG 2040
QY 88 GAATGATGTCAGATGAAACAAATCTCAGGAAAAAATTAAGTTATGGATGAAATAAA 147
DB 2041 GATTGTATATACGGGGATTATATATCCATGAGAAACGGAACTACAAATCTATGTCANA 2100
QY 148 CTGGCAAAACAACTTAGTCAGTCTGTATATCTACTCCAAATGAGACITTTCTGGAA 207
DB 2101 TACGCAAAACGTTTGAGCTATTCCTGATTAATTAATCTTAGATCCAAATTCGATTTAT 2160
QY 208 GATTGACATTCGTTATGATATATATCAATAGGATCCAAATCTATTTTAAAGAAA 267
DB 2161 AATTGATTCAGAGAGATGTTGTTAGAGATTAAGTATTTGATTTGAAATGGGAT 2220
QY 268 TTTCTACAGATGCGT-----GAGACACGACATATATGAACTCTATTTCCAAC 318
DB 2221 TTTGTATTCAAAGTATCATTTATTTTTCAGGTACCAATGATACCAATATCCACA 2280
QY 319 TATATCTGTCAAAAATGATGAGTCTAAATTAACCATATACGTTATGAGTAA 378
DB 2281 TATCTCTACAAAAATGATGAAATCCAACTCAAGAAATATACACGCTATTAAGTAAA 2340
QY 379 GGGTTGGGAGAGTAAAGATTGAATTAATGTTAACAAGTTACGGGAAAGAAAT 438
DB 2341 GGTATTCGAAAGTAGTACAGATTTAAGAGCTTATGTTGCTTATGATGACAAAACAT 2400
QY 439 GATGCTATCATGATATGTTCCAAATGATTTGGCTATATGACGCTTATCTTCATGTGA 498
DB 2401 AGACATTTGATGTTCTGATATATCTATTAACAGATATTTCTCCGAGAAATCATGTGA 2460
QY 499 GATTATCGCTGGAATCATCGTCTGATGTGAGCCAAAGGATTCCTACCAACAGAT 558
DB 2461 GAACCAAAATCGCTGCGCGCACMAACAATACCTG----- 2493
QY 559 GGATATGCTCCCGATATGATGATGATGCGCGCAAAATATAGATGAAAGCATGTGAGT 618
DB 2494 -----GATGAAATTCAGATTCAGATGATGTTGATGATGCAAGATGAAATTTTG 2541
QY 619 CAGCATGCTCATCATTTGATTTTTCATATGACACCGAGAGATGATCAATCAAT 678
DB 2542 TGTGATGGCATCATTTCTCTTAAATAGATATAGGTTTCAATATCATCAATGAA 2601
QY 679 GTAGTATTTGATGCTTATTAATAATTTCTAATCCAGATGATACGTTACAGTAGGAAT 738
DB 2602 TTAGGAATTTGGGTTGTTTAAATTTGACACATGAGAGATATGCGAAATTTGGAAT 2661
QY 739 CTAGAAATCATGAGAAAGAACCACTAACAGGTGAGATGCGCATGTAACAAAG 798
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QY 799 GAAAGAAATGAGAAACACATGAGAAACAACTTGGGAAACAAACAGCTATGAT 858
DB 2722 GAAAGAAATGAGAAACAGATTAACCACTGAGAAAGGAAACAGAGCAATTTATACA 2781
QY 859 CCAGCAAAACAGGCTGTAGATGATTTTACAAATGAACAGAGTTACACT-----AT 912
DB 2782 CGAGCAAAACAGGCTGTATCTTTTGGGAAATGACAAAGACTCTCACTTAAATA 2841
QY 913 CATATTACTTTAGATCATATTCAAAACGCTGATGACAGTCAATTCCTATGTA 972
DB 2842 GATGTTAATTTGCGGAAATTTGCGGCTGCAAGAAAGATTTGCAATCAATAGCGCAAGG 2901
QY 973 TACCATTAATTTGTTACCAATGCTCAGGTATGAATATGATGATATCAAGATTAAC 1032
DB 2902 TATATGATGTTATCTGTTGTTTCCAGGTGTAATCAACCCATTTTATCAAGTTAAGT 2961
QY 1033 GCAGTATCATGCAAGGTTATTAATTAATGATGACGAAATGTCATTAACAATGCTGAC 1092
DB 2962 GAGCAGATGACAAAGGATTTCAATTAATATGATGACAAAGATGTTGCTATGATGCA 3021
QY 1093 TTTACAAAGATTAACAGGATGACGCAACAGAAATGCGCGGTACAAACAAATGAT 1152

Db 3022 TTCCTCAATGCGTTATCCGATGTGATGTGAACATCTGACGTAAAGTACAAAGAAAT 3081
Qy 1153 GGAGCTTCAGTATTGTTCTTCTCAATTTGAGCGGGGGGTATCTCAAAACTTGATGCT 1212
Db 3082 GGGAAATACGATATGTTCTTAAACAATGGATGACAAAGTATTAACAAACCTAAACCTC 3141
Qy 1213 CAAGATCATCATGATATGTGTGTTACGTGATTCGCAAAAAAGAGACCTGGAAGAGG 1272
Db 3142 TATCAAGACCGGTGATATCTTACGTGAACGCCCGCAAGATAGATGGAGGAAGA 3201
Qy 1273 TATGTACAGATGATGATTTGATGAAGAGCAAGAAACATTAACTTCACTTTCCGA 1332
Db 3202 TATATTAACGATTAACGATGAAGAGGCACTCAATTAAGATTAAGTCAATGTGA 3261
Qy 1333 G-----AAGATATATGACAAACAGTGAAGGTATTC 1365
Db 3262 GTGATTGATGATCTTAATGCGTTTATATCCGTTATATTAACAAAGAACTGAATTC 3321
Qy 1366 CCAGAAAGTGAATCGTACGATTAAGAAATAGAGAAACGAAAGTACATTTATATAGAT 1425
Db 3322 CCAAGTACAGAAAGTGCATATAGAAATAGCGAAACAGAAAGAAATATTCCTGTAGAA 3381
Qy 1426 AGCATCGATGCTCTTGTATGCAAG 1450
Db 3382 AGTATAGATTATTTTGTATGGAAG 3406

RESULT 13
US-07-973-320-1
Sequence 1, Application US/07973320
Patent No. 5286486
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
TITLE OF INVENTION: No. 5286486e1 Bacillus thuringiensis Gene
TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,320
FILING DATE: 19921106
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/788,638
FILING DATE: '6-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA68.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3414 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis
STRAIN: dakota
INDIVIDUAL ISOLATE: HD511
IMMEDIATE SOURCE:
LIBRARY: Lamdagem (TM)-11 library of J.M. Fu
CLONE: 511
US-07-973-320-1
Query Match 17.8%; Score 299.8; DB 2; Length 3414;
Best Local Similarity 53.4%; Pred. No. 5.2e-66;
Matches 782; Conservative 0; Mismatches 602; Indels 81; Gaps 4;
Qy 28 AAAAAATCGTTAAATAGAACACAGATTTAGAAATAGATCAAGCGCCATTTCTATA 87
Db 1991 AGAAATGACCTCAAAAAATAGTACAGATTTAAAGTGACACAGTTTCAATTTTAGT 2040
Qy 88 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 147
Db 2041 GATTGATATACAGGGGATTTTATCCCAATAGAGAACGCAACTACAAATCTAGTCMA 2100
Qy 148 CTGGCAAAACAACTTAGCATCTCGTAATCTACTCCAAATGAGACTTTCTGGGAT 207
Db 2101 TAGCGAAAACGTTGAGCTATCCGTAATTAATCTTAGATCCCAATTCGATTTCTAT 2160
Qy 208 GATTGACATTCGGTAAATGATATATATATATATATATATATATATATATATATATAT 267
Db 2161 AATTCATCTGAGAGAAATGTTGATATGAGAAATGATATGATATGATATGATATGAT 2220
Qy 268 TTCTACAGATGCT-----GAGACAGACATATATGAACTTATTTTCAAC 318
Db 2221 TTGTATTAACAAAGTAACTATTTATTTTTCAGGTACCAATGATACAAATATCCAA 2280
Qy 319 TATATCTGCAAAAAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 378
Db 2281 TATCTTACCAAAAAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Qy 379 GGGTTTGGGAAAGTAAAGATTTGAAATTAATGATGATGATGATGATGATGATGATGAT 438
Db 2341 GGTTTTATCGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2400
Qy 439 GATGCTATCATGAATGTTCCAAATGATTTGGCTATATGACGCTTATCTTCAATGGA 498
Db 2401 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
Qy 499 GATTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 558
Db 2461 GAACCAATGCTCGCGCGGCAACAATACCTG----- 2493
Qy 559 GGATATGCTCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
Db 2494 -----GATGAAGATCCAAAGTTCAGAAATGATGATGATGATGATGATGATGAT 2541
Qy 619 CACATGCTATCAATTTGATTTTCAATTTGACACCGGAGAGTAAATCAATCAAT 678
Db 2542 TCTGATTCGATTTATTTCTTAATATATGATCAGGTCTTCAATCAATCAGAGAT 2601
Qy 679 GTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
Db 2602 TTAGGAATTTGGGTTGTTTAAATTTTCAATTAAGATTAAGATTAAGATTTTGAAT 2661
Qy 739 CTAAAGTCAATTAAGAAAGCACTAAACAGTGAAGATTTGGACATGTTGAACAAAG 798
Db 2662 CTAAAGTGAATTAAGATTTGGCCAGTTATTTGAAGAAACATTAAGCCGTGTAACGCCAA 2721
Qy 799 GAAAGAAATGAAACACACATGAGAGAAACGTTGGGAAACACAAACGCTATGAT 858
Db 2722 GAAACGAATGAGAAACAAAGTTAGCCCAATGACAAACGAAACAAACGATTTATCA 2781
Qy 859 CCAGCAAAACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
Db 2782 CGAGCAAAACAAAGCGTGAATATCTTTTTCGAAATGACAAAGACTCTCACTTAAATA 2841
Qy 913 CATATTACTTATGATTCATTTCAAAACGCTGATGATGATGATGATGATGATGATGAT 972

Db 2842 GATGTTACATTTTCGGAAATTCGGCTGCAGAAAGATTGTCATTCATACCGAAGTG 2901
Qy 973 TACCATTAATGGTTACCGAATGCTCAGATATGAATATGATATATCAAGATTAAAC 1032
Db 2902 TATATGTCATGTTATCTGTTGTTCCAGGTGTAATTCACCCATTTTTCACAGTTAAGT 2961
Qy 1033 GCACGTATCAGCAAGGTTATATTTATATGTCACGCAATGTCATAACAAATGTCAC 1092
Db 2962 GGGAGAGTACAAACGAGCATTTCAATTAATGATGACGAAAGTTGTGCGTATGTCGA 3021
Qy 1093 TTTACACAAGATTACAGGATGCGACGCAAGCAAGAAATGCGCGGTACACAAATGAT 1152
Db 3022 TTCTCAATGGCTTATCCGATTGATGTAACATCTGACGTAAAGCTACAGAGAAAT 3081
Qy 1153 GGAGCTTCAGTATTAATGTTCTATCAATTTGACGCGGGGTATCTCAAACTTGATGCT 1212
Db 3082 GGGATTAAGTATTTGTTGTTTAAACAATTTGGATGGCAAGTATTAAGAAAGTAAACCTC 3141
Qy 1213 CAAGTATCATGATATGTTGTTAGTGTGATTTGCCAAAAAGAACCTGGAAAGGG 1272
Db 3142 TATCAAGACCGTGGGATGCTCTTACGTGTACAGCGCGCAAGATGGAATTTGGGAAGGA 3201
Qy 1273 TATGTAAGCATGATGATGTTGTAATGGAAGCAAGCACTTAAGTTCCTTGCGCA 1332
Db 3202 TATATTAACGATTACTGATGAGAGGCGCATACAGATCAATTGAGATTACTGATGTGA 3261
Qy 1333 GA-----AGGATATATGACAAAAACAGTAGAGTATTC 1365
Db 3262 GAGATTGATGATCTTAATGCGTTTATATCCGTTATATTAACAAAGAACTGGAATTTCTC 3321
Qy 1366 CCAGAAAGTATGCTGTGATCGAATTGAATAGAGAAACCGAAGTACATTTTATATAGT 1425
Db 3322 CCAGATACAGAGAAAGTGCATATAGAAATAGCGCAAGAGAAATATTTCTGTAGAA 3381
Qy 1426 AGCATCGAGTCTGTTGATGCAAG 1450
Db 3382 AGTATGAGATTATTTTGTATGGAAG 3406

RESULT 14

US-08-315-468-3
Sequence 3, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Ponceirada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73, C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: 50C
IMMEDIATE SOURCE:
LIBRARY: LambdaGem-11 (cm) library of L. Ponceirada
CLONE: 50C(b)
US-08-315-468-3
Query Match 17.0%; Score 286.6; DB 2; Length 3507;
Best Local Similarity 54.7%; Pred. No. 1.2e-62;
Matches 729; Conservative 0; Mismatches 529; Indels 75; Gaps 5;
Qy 22 ACTACGAAATATACGTTAAATATGAAACGACAGTTATGAAATGATCAAGCGCCATT 81
Db 2038 AATACAAAAGATGATTCAGCCAGCGTGAACGATTATGAAATCAACCGGCCAAC 2097
Qy 82 TCTATGATGATGATGTCAGATGAACAAATCCTCAGAAAAATATATGTTATGAGTGA 141
Db 2098 TTATGGAATGCTTATCGATGATTTGTATTCATTAATGAAAAAGATGTTATTTGATGA 2157
Qy 142 ATAAACTGGCAAAACCTAGTCAGTCTGTATCTACTCAAAATGAGACTT---- 197
Db 2158 GTGAGAGAGCAAAACGACTTAGCGAGGACGAACTTACTCAAGATCCAGATTTCCAA 2217
Qy 198 -----TTCTGGAAATGATTTGACATTCGTTATGATATTTATCATAGATCCATAT 249
Db 2218 GAGATTAATGAGAAATGAGATGACGCGCAAGTACGGAAATGAGTTATGAAGGGAT 2277
Qy 250 CCTATTTTAAAGAAATTTCTACAGATCGGTGAGACGAGACATATATGAACTCTA 309
Db 2278 GCTGATTTCAAGGCGTTATCTACGCCCTACAGGTGCGAGGAAATGATACGGAACG 2337
Qy 310 TTCCAACTATATCTGTCAAAAAATAGATGATTAATTTAAACCATATACAGTTAT 369
Db 2338 TATCCAGATATCTGATATCAAAAAAGTATGAGAAAGTATTTAAACCATATACAGTTAT 2397
Qy 370 CGAGTAAAGGTTTGTGGAAAGTATGAAGTTTGAATTTATGATTAATGATTAACGTTACGG 429
Db 2398 AGACTGAGAGGATTTGTGGAAAGTATGCAAGGATTTGAATTTATACGTTGTGACCAA 2457
Qy 430 AAGAAATTTGATGATCATGATGAAATGTTCCAAATGATTTGGCTATATGAGCTATCT 489
Db 2458 A-----CGAATCGAATTTGTAATAAATGATACAGATGATTTATGCGCAAGTGA 2505
Qy 490 TCATGTGAGATTAATCGGTGTAATCATGCTCATGATGTTGAGCCAAAGGATATCTTACA 549
Db 2506 CCTCTGTAACAAATGATGATGA-----A 2530
Qy 550 CCAAGATGATGATGCTCCGATATGATGATGATGATGATGATGATGATGATGATGATGAT 609
Db 2531 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2590
Qy 610 GTGAAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669

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